WEST

Create A Case

Select?	Database	Query	Plural	Op	Thesaurus	Set Name
Ø	USPT	anti-tumor antibody	YES	ADJ	ASSIGNEE	Li`.
Ø	USPT	anti-tumorigenic antibody	YES	ADJ	ASSIGNEE	L2
v	USPT	antibody and anti-tumorigenic activity	YES	ADJ	ASSIGNEE	L3

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Rules for naming Cases

- Case names can only contain alphanumeric characters including underscore ().
- Any other special characters or punctuation characters will be automatically removed prior to saving the case.
- All white space characters will be replaced by an underscore.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

July 8, 2003, 16:08:55; Search time 47.5 Seconds (without alignments) 53.300 Million cell updates/sec Run on:

US-09-824-647-3 96 Perfect score: Title:

1 KKVIAPRRLPDPQILKSDT 19 Sequence:

BLOSUM62 Scoring table:

908470 seqs, 133250620 residues Searched:

Gapop 10.0 , Gapext 0.5

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/gcgdata/geneseq/geneseqp-embl/AA1980.DAT /gcgdata/geneseg A_Geneseq_101002:*

/SIDS2

/qcqdata/qeneseq,

/gcgdata/geneseg/genesegp-embl/AA1994.DAT /qcqdata/qeneseq /gcgdata/geneseg

/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA2000.DAT /gcgdata/geneseq/geneseqp-embl/AA1998.DAT /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Mouse GP88 autocri	Mouse epithelin pr	Mouse GP88 autocri	Mouse granulin/epi	Rat epithelin prec	Novel human diagno	Human ADAM8. Homo	Human PRO1686 poly	Human GP88 autocri	Human calbastatin
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		5478	1327	5474	0520	1325	7964	0251	5156	5480	3298
	0	AW8	VAR1	AW8	AE2	AAR14325	PG0.	AB2	AUB.	LAW8	LAMI
	a I	. ~	7	0	3	7	7	22	<u>ر</u>	0	8
	EQ 1	. 7	_			_	~		7	-	_
	Query Match Length DB	19	583	289	583	589	9	824	824	15	29
	ch	0.	0			64.6	0.	6.	6.	80	8
ф	Que M at	100	100	92	. 92	9	4	4	47	45	45
	Score	96	96	89	83	62	47	46	46	44	44
	Result No.	1	7	6	4	S	9	7	æ	σ	10

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Human protoin secui	process	Carpastati	Human epithelin pr	Granulin sequence.	Human GP88 autocri	Human granulin/epi	Human cancer assoc		Arabidopsis thalia		Arabidopsis thalla	¥			Human POLY3 protei	Amino acid sequenc	Human cardiac myos	Human cardiac myos	Human cardiac myos		Human cardiac myos	Human kinase PKIN-	Human POLY4 protei	Human protein kina	Drosophila melanog	Propionibacterium	Novel human diagno	_	Novel human diagno	α.	Novel human diagno	Amino acid sequenc	3		Novel human diagno
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,	70	97	1.2	14	20	73	21	21	21	21	21	22	23	23	23	22	23	23	23	23	23	23	23	22	22	22	22	23	22	22	22	22	22	23	22
413	4.50	403	593	593	593	593	621	108	131	142	148	154	595	595	565	296	296	296	296	296	296	965	965 /	612	692	. 57	97	97	255	298	321	416	416	440	501
u . *	0.0	. n. a	٠			45.8	45.8	44.8	44.8	44.8	. 44.8	44.8	44.8	44.8	44.8	4	44.8	44.8	44.8	44.8	44.8	٠.	44.8	•	٠			43.8			43.8		•	43.8	43.8
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;	11	77	13	14	15	16	17	18	19	20	. 21	. 22	23	24	25	26	27	28	29		31				35			38	39	40	. 41	42	. 43	44	. 45

ALIGNMENTS

AAW85478 standard; Peptide; 19 AA. 15-MAR-1999 (first entry) AAW85478; RESULT 1 AAW85478

Mouse GP88 autocrine growth factor antigenic peptide K19T.

GP88; granulin; epithilin; mouse; growth factor; autocrine; tumour; cancer; viral infection; antagonist; therapy; diagnosis; antigen; antibody.

Mus sp.

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W09852607-A1

26-NOV-1998.

98WO-US10555. 22-MAY-1998;

97US-0991862. 97US-0863079. 16-DEC-1997; 23-MAY-1997;

(SERR/) SERRERO G.

Serrero G;

WPI; 1999-045276/04.

Composition containing antagonist of growth factor GP88 - useful for treating cancer and viral diseases and also for diagnosing disease

à g

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ET-1 is a bifunctional growth regulator, capable of stimulating the growth of some cell types while inhibiting the growth of others. ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory bioactivity. In contrast, however, ET-2 is apparently not capable of eliciting the growth stimulatory activity characteristic of ET-1 and, in fact, artagonises this ET-1 activity. See also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20.
                                                                                                                                                                                                                           New cysteine-rich growth modulating proteins, epithelins - useful as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344..362
/note= "K19T peptide, used to raise antibody"
562..575
/note= "S14R peptide, used to raise antibody"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "P12T peptide used to raise antibody"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GP88; granulin; epithilin; mouse; growth factor; autocr.
cancer; viral infection; antagonist; therapy; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 96; DB 12; 100.0%; Pred. No. 1.4e-06;
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                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 23; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         344 KKVIAPRRLPDPQILKSDT 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW85474 standard; Protein; 589
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97US-0863079.
                                                                               (BRIM ) BRISTOL-MYERS SQUIB
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                                                                                                                   Shoyab M, Plowman GD;
                                                                                                                                                                 WPI; 1991-325168/44.
N-PSDB; AAQ14340.
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Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    589 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-DEC-1997;
23-MAY-1997;
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                                                                             This is the amino acid sequence of peptide K19T, comprising amino acid residues K344-T362 of murine GP88 (see AAW85474). GP88 is an kDa glycoprotein autocrine growth factor that is expressed in a tightly regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which acts as a stringently required growth stimulator for the tumorigenic cells. K19T was used to raise neutralising antibodies to GP88. Antagonists to GP88, such as anti-GP88 antibodies, are used to treat diseases associated with increased expression of GP88, particularly cancer but also viral infections. Anti-GP88
                                                                                                                                                                                                                                                                                              antibodies can also be used as diagnostic reagents and to deliver toxins or other compounds to GP88-expressing cells.
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0
                                                                                                                                                                                                                                                                                                                                                                                                 Length 19;
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                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 96; DB 20;
100.0%; Pred. No. 3.9e-08;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ET; growth regulation; inhibition; stimulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label- EP /note= "claim 27, page 56" | 515.570 | /label- EP /note= "claim 28, page 56"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label- precursor
/note- "claim 21, page 55"
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/label- EP-1
/note- "claim 22, page 55"
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/note= "claim 25, page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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/note- "claim 23,
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from altered GP88 expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse epithelin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .261
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                                                                                                                                                                                                                                                                                                                                                              Sequence
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Indels

Length 589;

us-09-824-647-3.rag

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Rattus rattus.
                                                  23-MAY-1997;
08-DEC-1999;
 28-FEB-2002
                                                                                                                 Serrero G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR14325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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antineoplastic; antioestrogen therapy; skin cancer.
                                                                                                                                                                                       glycoprotein autocrine growth factor and epithilin/granulin precursor that is expressed in a tightly regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which acts as a stringenily required growth stimulator for the tumorigenic cells. Inhibition of GPBB expression or action in the tumorigenic cells. Inhibition of the tumorigenic properties of the overproducing inhibition of the tumorigenic properties of the overproducing cells. Murine GPBB CDNA (see AAVB2824) was obtained from the highly tumorigenic properties of the overproducing culls. Antagonists to GPBB are used to treat cancer but also viral infections. Fragments of GPBB are used to
                                                                                                  Composition containing antagonist of growth factor GP88 - useful for treating cancer and viral diseases and also for diagnosing disease from altered GP88 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note- "Regions used as antigens to raise anti-GP88 antibodies"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     562..575
/note= "Regions used as antigens to raise anti-GP88
antibodies"
                                                                                                                                                                                                                                                                                                                                              reagents and for delivering toxins or other compounds to GP88-expressing cells) and to screen for antibodies. Methods are provided for diagnosing disease, or determining susceptibility disease, resulting from altered GP88 activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                      cancer but also viral infections. Fragments of GPBB are used raise specific antibodies (used as antagonists, as diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 589;
                                                                                                                                                                             This is the amino acid sequence of murine GP88, an 88 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 89; DB 20; Length 58
Pred. No. 1.7e-05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse granulin/epithelin precursor (GP88) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /hote- "Encoded by ACA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Unknown
/note= "Encoded by ATG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE20520 standard; Protein; 589 AA.
                                                                                                                                                   Example 5; Fig 8A-D; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     344 KKVIAPLRLPDPQILKSDT 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KKVIAPRRLPDPQILKSDT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                      92.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 92.7
Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..362
                                                           WPI; 1999-045276/04.
N-PSDB; AAV82824.
                                                                                                                                                                                                                                                                                                                                                                                                            589 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
           (SERR/) SERRERO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2002025543-A1
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                                     Serrero G;
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE20520;
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AAE20520
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The invention relates to a method for diagnosing tumourigenicity in a human. The method comprises obtaining a biological sample containing cells from the patient, detecting 9888 in the cells of the sample, and determining the number of GP88 positive cells in the sample, and determining the ratio of GP88 positive cells to the total number of cells in the sample. The invention also relates to a method for determining if a human patient is resistant to the antineoplastic effects of antioestrogen therapy. The method is useful for diagnosing tumourigenicity in a sample, such as blood, serum, plasma, urine, nipple aspirate, cerebrospinal fluid, liver, kidney, breast, bone, brain, lung, colon, or skin cancer. The method can be used to treat or prevent re-occurrence of cancer in a patient, by administering tamoxifien if the sample contains less than 10 % GP88, or less than 5 % GP88 positive
                                                                                                                                                                                                                                                                                                                          Diagnosing tumorigenicity in a human, comprising obtaining a cell sample, detecting GPB8 in the cells, and determining the number of GPB8 positive cells in the sample -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 89; DB 23; Length 589;
Pred. No. 1.7e-05;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ET; growth regulation; inhibition; stimulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   page 54"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note-
280..335
/label= EP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR14325 standard; Protein; 589 AA.
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/note= "claim 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= precursor
/note= "claim 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Fig 8; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KKVIAPRRLPDPQILKSDT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.78;
15-JUN-2001; 2001US-0880842.
                                                   970S-0863079.
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/label= EP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JAN-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.79
Best Local Similarity 94.77
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat epithelin precursor.
                                                                                                                                                                                                                                               WPI; 2002-267529/31.
N-PSDB; AAD32849.
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                                                                                                                                       (SERR/) SERRERO G.
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us-09-824-647-3.rag

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30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                               diagnostics,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human ADAM8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB20251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ద
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ET-1 is a bifunctional growth regulator, capable of stimulating the growth of some cell types while inhibiting the growth of others. ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory bloactivity. In contrast, however, ET-2 is apparently not capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bioactivity. In contrast, however, ET-2 is apparently not capable of eliciting the growth stimulatory activity characteristic of ET-1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in fact, antagonises this ET-1 activity.
See also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New cysteine-rich growth modulating proteins, epithelins - us as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 12; Length 589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 62; DB red. No. 0.26
                                                                                                                                                        label- EP
note- "claim 17, page 54"
                                                       page 54"
"claim 14, page 54"
                                                                                                                                                                                                                                           'note= "claim 18, page 55"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #7955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG07964 standard; Protein; 650 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 18; 97pp; English.
                                                                                               /label= EP
/note= "claim 16,
                                                       claim 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              344 KKVTASLSLPDPQILKND 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KKVIAPRRLPDPQILKSD 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 64.6%;
Best Local Similarity 72.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BRIM ) BRISTOL-MYERS SQUIB.
                                                                                                                                                                                                                                                                                                                                                                91WO-US02321
                                                                                                                                                                                                                                                                                                                                                                                                        910S-0083796
900S-0504508
                                      'label" EP
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                                                                                                                                                                                               515..570
                                                                                                                                       140..495
'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plowman GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1991-325168/44.
N-PSDB; AAQ14338.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                03-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                        .3-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                           03-APR-1990;
                                                                                                                                                                                                                                                                                 W09115510-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shoyab M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG07964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                   Peptide
                   Peptide
                                                                            Peptide
                                                                                                                                       Peptide
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polypeptide (II) sequences (I) is useful as hybridisation probes, polypeptide (II) sequences (II) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase are also used in disgnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in disagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and to produce other types of data and products dependent on DNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                liagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADAM8; human; tumour; cancer; therapy; diagnosis; antitumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 650;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID No 38323; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB20251 standard; Protein; 824 AA
                                                                                                                                                                                              Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.0%;
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31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|| ||| ||:|
291 LAPTRLPQPQVL 302
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Best Local Similarity
                                                                                                                                                                                                                                                                       WPI; 2001-639362/73.
N-PSDB; AAS72151.
                                                                                                                                                                                              Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             650 AA;
                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200109189-A2.
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Hillan KJ; Stone DM;

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polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, stromal and blastocoelic disorders, inflammatory, immune and angiogenic disorders. The polynucleotide sequences are also useful in gene therapy. Angels 18-AAU86162 represent the human PRO polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ranulin; epithilin; human; growth factor; autocrine; tumour; viral infection; antagonist; therapy; dlagnosis; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to the isolation of novel human PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumours, leukaemias and lymphoid malignancies, inflammatory, anglogenic and immunologic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.9%; Score 46; DB 23; Length 824;
43.8%; Pred. No. 1.1e+02;
Live 6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human GP88 autocrine growth factor antigenic peptide E19V.
                                                                                                                                                                                                                                                                                         Goddard A, Godowski PJ, Gurney AL,
Pan J, Pitti RM, Roy MA//\Smith V,
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW85480 standard; Peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 61; Fig 58; 302pp; English.
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30 EVVLPRRLPGPRVRRA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 KVIAPRRLPDPQILKS 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US10555.
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                                                                                                                                           99WO-US21090
99WO-US28313
                                                                                                                                                                                                                            2000WO-US00219
                                                                                                    99US-151689P
                                                                                                                                                                                       99WO-US28301
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                                                                                                                     99WO-US20111
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                                                                                                                                                                                                                                                                   (GETH ) GENÈNTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-205967/26.
N-PSDB; ABK40282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          824 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GP88; granulin;
                                                                                                                                                                                                                                                                                                               Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                     Marsters SA,
Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAY-1998;
                                                                                                                                                                                                                                05-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-DEC-1997;
                                                                                                  31-AUG-1999;
01-SEP-1999;
                                                                                                                                           15-SEP-1999;
30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-NOV-1998.
                                                                                  7-AUG-1999
                                                                                                                                                                                         -DEC-1999
                                                                                                                                                                                                        -DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW85480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW85480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                The present sequence is that of human ADAMB, a protein containing a metalloprotease and a disintegrin domain. The ADAMB gene (see MER3037) is amplified in the genome of ceals of certain breast, lung and colon cancers. Such gene amplification is associated with the overexpression of the gene product and contributes to the overexpression of the gene product and contributes to the overexpression of the gene product and contributes to the overexpression of the gene product and contributes to the overexpression of the diagnosis and/or treatment or prevention of certain cancers, and acts as a predictor of the prognosis of tumour certain cancers, and acts as a predictor of the prognosis of tumour converses through the extracellular matrix or possibly in the monocytes through the extracellular matrix or possibly in the processing of cytokines or other chemotactic molecules. Increased which the near tumour cells may provide a means by which tumour cells invade tissue or form metastases. Targeting such a molecule with an antibody or another molecule that block, inactivates or othe of tissue results in a clinically relevant antitumour therapeutic. ADAMB polypeptides can be used to raise ADAMB -specific antibodies, and to screen for inhibitor compounds, seed to inhibit the growth of tumour cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
leukaemia; neuronal disorder; stromal disorder; blastocoelic disorder;
inflammatory disorder; immune disorder; anglogenic disorder;
cytostatic; neuroprotective.
                                                                                                                                                                                     Antibodies against ADAM8 polypeptides, useful e.g. for diagnosis and treatment of tumours and inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.9%; Score 46; DB 22; Length 82
43.8%; Pred. No. 1.1e+02;
Live 6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU86156 standard; Protein; 824 AA.
                                                                                                                                                                                                                                                  Disclosure; Page 5; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : |: ||||| |: :: 30 EVVLPRRLPGPRVRRA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-123972P.
99US-133459P.
99WO-US12252.
99US-140650P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-FEB-2000; 2000WO-US03565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-0505028
99US-0146217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human PR01686 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 43.89
Matches 7; Conservative
                                                                              Bodary SC, Fisher KL;
                                       (GETH ) GENENTECH INC
                                                                                                                   WPI; 2001-182943/18.
                                                                                                                                             N-PSDB; AAF30377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200153486-A1
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11-MAY-1999;
02-JUN-1999;
22-JUN-1999;
28-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUL-2001.
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RESULT 8 AAU86156

δ QQ ö

Gaps

us-09-824-647-3.rag

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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                           This peptide comprises a B-cell epitope from a calpastatin isoform (see AAM18394) found in human testis and sperm, but not in other tissues. Calpastatin is an inhibitor of the cystelne proteadse calpain. The B-cell epitope, or a shortened B-cell epitope (see AAM19298), can be linked to a carrier comprising a universal T-cell epitope from tetanust coxold (see AAM18295 and AAM18295) to produce an immunogen (see AAM1830). The B-cell epitope or immunogen can be produced by chemical synthesis or as accombinant peptides in host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                          cells. They are useful as contraceptive vaccines that inhibit fertilisation of an egg by sperm. The B-cell epitope can also be used to detect specific antibodies in body fluids, the presence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamamoto J;
useful in contraceptive vaccines for males or females, and for diagnosing infertility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saito K, Ya
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                          these antibodies being indicative of infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; SEQ ID 15310; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 18;
6.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isogai T, Nishikawa T, Hayashi K, S
Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human protein sequence SEQ ID NO:15310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ź
                                                                                     Claim 17; Page 68; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB94550 standard; Protein; 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99JP-0300253.
2000JP-0118776.
2000JP-0183767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUL-2000; 2000EP-0116126.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 44.4%;
watches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUL-1999; 99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JUN-2000; 2000JP-0241899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ull-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB94550;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
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ID AAB9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
            Composition containing antagonist of growth factor GPBB - useful for treating cancer and viral diseases and also for diagnosing disease from altered GPBB expression
                                                                                                                                                                                                                                                                                                                                                           comprising amino 175). GP88 is an 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New testis-specific isoform of calpastatin - and derived immunogens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protease inhibitor; immunogen; diagnosis; epitope;
                                                                                                                                                                                                                                                                                                                                                                                acid residues E340-V364 of human GPBB (see AAWB5475). GPBB is an EXDA glycoprotein autocrine growth factor that is expressed in a tightly regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which acts as a stringently required growth stimulator for the tumorigenic cells. E19V was used to raise neutralising antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumorigenic cells. E19V was used to raise neutralising antibodies to GP88. Antagonists to GP88, such as anti-GP88 antibodies, are used to treat diseases associated with increased expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPB8, particularly cancer but also vital insection. ....antibodies can also be used as diagnostic reagents and to deliver toxins or other compounds to GPB8-expressing cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.8%; Score 44; DB 20; Length 19;
55.6%; Pred. No. 4.4;
tive 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                         This is the amino acid sequence of peptide E19V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Calpastatin; testis; human; calpain; vaccine; contraceptive; infertility; B-cell; B-lymphocyte.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                          Example 8; Page 45; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4..17
/note= "Claim 18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human calpastatin B-cell epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW18298 standard; Peptide; 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KKVIAPRRLPDPQILKSD 18
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            23-MAY-1997; 97US-0863079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 55.6
ses 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weinberg PO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-385110/35.
                                                                                                                                                        WI; 1999-045276/04
                                                             (SERR/) SERRERO G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9726001-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JUL-1997
                                                                                                              Serrero G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW18298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
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Gaps

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the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a sequence and an oligonucleotide comprising a sequence, where the oligonucleotide comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs asally without any specialised methods. AM403166 to AM41878 and AM418731 to AM418742 represent human cDNA sequences; MAB92446 to
                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                               AB95893 represent human amino acid sequences, and AAH13629 to AAH13632 epresent oligonuclectides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New testis-specific isoform of calpastatin - and derived immunogens, useful in contraceptive vaccines for males or females, and for diagnosing infertility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Calpastatin; testis; human; calpain; protease inhibitor; immunogen; vaccine; contraceptive; infertility; diagnosis; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This polypeptide comprises an isoform of human calpastatin found
                                                                                                                                                                                                                                                                                                                                                                                                                                   ő
                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 22; Length 413;
Pred. No. 1.10+02;
1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 426..454
/note= "B-cell epitope (Claim 17)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "B cell epitope (Claim 18)"
                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 16; Page 39-41; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human calpastatin (clone C-2 product).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW19394 standard; Protein; 463 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KKVIAPRRLPDPQILKSD 18
                                                                                                                                                                                                                                                                                                                                                                                           45.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0586592.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NOUN ) UNIV NORTHWESTERN.
                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Weinberg PO;
                                                                                                                                                                                                                                                                                                                    of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-385110/35.
N-PSDB; AAT72643.
                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                          413 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9726001-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soldberg E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4-JUL-1997
                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW19394;
                                                                                                                                                                                                                                                                                   AAB95893
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Peptide
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Gaps
in sperm and testis but not in other tissues. It can be produced in transformed host cells using isolated cDNA clone C-2 (see AAT72643).

A B-cell epitope (see AAW18288-99) of this calpastatin isoform can be used to prepare an immunogen (see AAW18300) useful as a male or female contraceptive vaccine that inhibits egg fertilisation. The protein and B-cell epitope can also be used in methods for detecting specific antibodies in body fluids, the presence of these antibodies being indicative of infertility.
                                                                                                                                                                                                        ö
                                                                                                                                                                           Length 463;
                                                                                                                                                                                                        Indels
                                                                                                                                                                         Score 44; DB 18; L
Pred. No. 1.2e+02;
; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ET; growth regulation; inhibition; stimulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-
124.180
/label EP
-+a- "claim 5, page 53"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= precursor
/note= "claim 1, page 53"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= EP
/note= "claim 8, page 55"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note- "claim 2, page 53"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "claim 3, page 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note- "claim 7, page 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "claim 4, page 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                      AAR14326 standard, Protein; 593 AA
                                                                                                                                                                                                                                                          : | | | | | | : | : | : | : EKKHTPRRRPEPKIIPSE 448
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                                                                                                                                                                                                                                        1 KKVIAPRRLPDPQILKSD 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82..337
label= EP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106..262
| Tabel = EP-2
                                                                                                                                                                           45.8%;
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                                                                                                                                                                                         Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91US-0083796
90US-0504508
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label = EP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   label- EP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human epithelin precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note=
                                                                                                                                               463 AA;
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03-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9115510-A.
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                                                                                                                                                                                                                                                                       431
                                                                                                                                                Sednence
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                                                                                                                                                                           Query Match
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Query Match
Best Local Similarity 55.6%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                593 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAV82825
                                                                                                                                                                                                                                                                                    Homo sapiens.
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23-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAY-1998;
                                                                                                                                                                                                15-MAR-1999
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                                                                                                                                                                        AAW85475;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                        RESULT 15
                                                                                                                                   AAW85475
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                                                                                                                     the growth of some cell types while inhibiting the growth of others. ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory bloactivity. In contrast, however, ET-2 is apparently not capable of eliciting the growth stimulatory activity characteristic of ET-1 and, in fact, antagonises this ET-1 activity.

See also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20.
                                                                                                                                                                                                                                                             Gaps
                                   New cysteine-rich growth modulating proteins, epithelins - useful as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 granulin inhibits keratinocytes and is useful in formulations promoting the healing of wounds.
                                                                                                             capable of stimulating
                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New cystine rich granulin peptide(s) from leucocyte(s) - are keratinocyte inhibitors useful topically for wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Granulin; keratinocytes; wound healing; inhibition; peptide;
                                                                                                                                                                                                                                   Length 593;
                                                                                                                                                                                                                       Score 44; DB 12; Length 59.
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Glycine encoded by CAG."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Valine encoded by ATG."
                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                             ET-1 is a bifunctional growth regulator,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Figure 4c; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     AAR48673 standard; Protein; 593 AA.
                                                                                     Disclosure; Fig 22; 97pp; English.
                                                                                                                                                                                                                                                                                                18
                                                                                                                                                                                                                                 Query Match
Best Local Similarity 55.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                    1 KKVIAPRRLPDPQILKSD
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                                                                                                                                                                                                                                                                                                                                                                                                                      22-APR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 granulocytes; leucocytes.
WPI; 1991-325168/44.
N-PSDB; AAQ14339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NPI; 1993-320328/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 452
                                                                                                                                                                                                            593 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SOLO/) SOLOMON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Solomon S;
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                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                RESULT 14
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ID AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is the amino acid sequence of human GPBB, an BB kDa glycoprotein autocrine growth factor and epithilin/granulin precursor that is expressed in a tightly regulated manner in normal cells, is overexpressed and unrequiated in highly tumorigenic cells derived from normal cells, and which acts as a stringently required growth stimulator for the tumorigenic cells. Inhibition of GPBB expression or action in the tumorigenic cells results in an inhibition of the tumorigenic properties of the overproducing cells. Antegonists to GPBB are used to treat diseases associated with increased expression of GPBB, particularly cancer but also viral infections. Fragments of GPBB are used to raise specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GP88; granulin; epithilin; human; growth factor; autocrine; tumour; cancer; viral infection; antagonist; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibodies (used as antagonists, as diagnostic reagents and for delivering toxins or other compounds to GRB8 expressing cells) and to screen for antibodies. Methods are provided for diagnosing disease, or determining susceptibility to disease, resulting from
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/note= "El9V peptide used to raise antibody"
566..579
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                     Length 593;
                                                                                                Indels
Score 44; DB 14; L/Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human GP88 autocrine growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                              AAW85475 standard; Protein; 593 AA
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                                                                                                1;
                                                                                                                                                                                                           346 EKAPAHLSLPDPQALKRD 363
                                                                                                                                                                   1 KKVIAPRRLPDPQILKSD 18
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970S-0863079.
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Length 593;

DB 20;

45.8%; Score 44;

0; Gaps Best Local Similarity 55.6%; Pred. No. 1.6e+02; Matches 10; Conservative 1; Mismatches 7; Indels

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Search completed: July 8, 2003, 16:24:13 Job time : 49.5 secs

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1 KKVIAPRRLPDPQILKSDT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New York
                   FEATURE:
NAME/KEY: PEPTIDE
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/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/AB_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
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GenCore version 5:1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Perfect score:
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                                        OM protein
                                                                                                                     Sequence:
                                                                                                                                                                       Searched:
                                                           Run on:
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No.
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Appli
Appli
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Sequence Sequence Sequence Sequence Sequence
US-09-152-060-84

US-08-527-236-6

US-08-46-517-6

US-08-463-172-6

US-08-463-772-6

US-08-464-517-23

US-08-464-517-23

US-08-246-3618-6

US-08-246-3618-772-23

US-08-463-772-23
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US-09-336-536-28
US-08-979-424-1
US-08-706-216-6
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US-08-975-762-69
US-09-295-028-69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08991862, Patent No. 6309826
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GENERAL INCORMATION:
APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REPERENCE: 2996.488/P001-A
CURRENT APPLICATION NUMBER: US/08/991,862
CURRENT FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/863,862
EARLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VET: 2.0 SEQ ID NO 3 LENGTH: 19 TYPE: PRT ORGANISM: mouse granulin

LOCATION: (1)..(19) contains the contains of mouse GP88 used to raise the CYHER INFORMATION: Internal against the GP88 used in the OTHER INFORMATION: immunoaffinity step.

Gaps ö ; Score 96; DB 4; Length 19; Pred. No. 1.3e-09; 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.0%;
Matches 19; Conservative 0

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APPLICANT: Shoyab, Mohammed

PRELICANT: Plowman, Gregory D.

TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH

TITLE OF INVENTION: MODULATING PROTEINS US-07-668-648-6; Sequence 6, Application US/07668648; Sequence 6, Application US/07668648; Patent No. 5416192; GENERAL INFORMATION:

E: Pennie & Edmonds 1155 Avenue of the Americas

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Length 589;
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Patent No. 5965723
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Showman, Gregory D.
TITLE OF INVENTION: MODULATING PROTEINS
TITLE OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,333
FILING DATE: 27-APR-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 96; DB.2; Best Local Similarity 100.0%; Pred. No. 6.3e-08; Matches 19; Conservative 0; Mismatches 0;
                                                                                                                                                 6.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
TELECOMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
                                                                                                                          Query Match 100.0%; Score 96; Best Local Similarity 100.0%; Pred. No. 6 Matches 19; Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-WAR-1991
ATTORNEY/AGENT INFORWATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application PC/TUS9102321 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: (
: 589 amino acids
amino acid
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-431-333-6
                                                       , MOLECULE TYPE: protein US-08-429-998-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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Patent No. 5885961
GENERAL INFORMATION:
APPLICANT: Showman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STRREF: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 589;
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,998
FILING DATE: 27-APR-1995
CLASSIFICATION NUMBER: US 07/668,648
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 0-0011
                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,648
FILING DATE: 19910819
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 96; DB 1; Best Local Similarity 100.0%; Pred. No. 6.3e-08; Matches 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                           CLASSIFICATION: 514
ATTORNET/AGENT INFORMATION:
NAME: Mistock, S. Leslie, 872
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEPAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 589 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-668-648-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                            COMPUTER READABLE FORM:
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    COUNTRY:
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NOVEL CYSTEINE-RICH GROWTH
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APPLICATION NUMBER: US/07/668,648 FILING DATE: 19910819
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                                  Sequence 2, Application US/07668648
Patent No. 5416192
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: PLOwman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CY
TITLE OF INVENTION: MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 62;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               344 KKVTASLSLPDPQILKND 361
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                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: THEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,87.
REFERENCE/DOCKET NUMBER: 5
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (212)790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 589 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212) 869-9741 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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ADDRESSEE: Pennie &
                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
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Best Local Similarity
Matches 13; Conserva
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: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                   ZIP: 10036
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APPLICANT: SETECT, dinette
TITLE COF INVENTION: 88 ADA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REPERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/08/991,862
CURRENT FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/863,862
EARLIER FILING DATE: 1997-05-23
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 Gregory D. EPITHELINS: NOVEL CYSTEINE-RICH GROWTH MODULATING PROTEINS
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                                                                                                                                                                                                                                                                         SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/0231
FILING DATE: 19910403
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: POOL' BILAN W.
REGISTRATION NUMBER: 32,928
REFRENCE/POOCKET UNBER: ON0071A-PC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.3e-08;
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Pred. No. 9e-07;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                     NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
STREET: 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 96;
Pred. No. 6
                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Mouse epithelin/granulin US-08-991-862-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08991862
Patent No. 6309826
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Best Local Similarity 100.0%;
Matches 19; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (206)448-4775
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 589 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 92.7
Best Local Similarity 94.7
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 17 SOFTWARE: Patentin Ver.
                                                                                                                              CITY: Seattle
STATE: Washington
APPLICANT: Plowman IITLE OF INVENTION: FITLE OF INVENTION:
                                                                                                                                                                   COUNTRY: USA
ZIP: 98121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 2
LENGIH: 589
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ð a CURRENT APPLICATION DATA:

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Gaps

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us-09-824-647-3.rai

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APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 2996.488/P001-A
CURRENT APPLICATION NUMBER: 05/08/991,862
CURRENT FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/863,862
                                                                                                                                                                                                                                                                                           APPLICANT: Shoyab, Mohammed

PRILCANT: Plowman, Gregory D.

TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH

TITLE OF INVENTION: MODULATING PROTEINS
                 Length 589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
AURIENT APPLICATION DATA:
AUBLICATION NUMBER: PCT/US91/02321
FILING DATE: 19910403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 62; DB 5;
Pred. No. 0.025;
                   Score 62; DB 2;
Pred. No. 0.025;
                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Bristol-Myers Squibb Company
STREET: 3005 First Avenue
                                                                                                                                                                                                                                             Sequence 2, Application PC/TUS9102321
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-991-862-6; Sequence 6, Application US/08991862; Patent No. 6309826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   344 KKVTASLSLPDPQILKND 361
                                                                                                                                           344 KKVTASLSLPDPQILKND 361
                                                                                                      1 KKVIAPRRLPDPQILKSD 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FELECOMMUNICATION INFORMATION TELEPHONE: (206)728-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KKVIAPRRLPDPQILKSD
                     64.6%;
ilarity 72.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 64.6
Best Local Similarity 72.2
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington
                        Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Seattle
STATE: Washing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 62; DB 2; Length 589;
Pred. No. 0.025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872.
REFERENCE/DOCKET NUMBER: 5624-161-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Pennie & Edmonds
1155 Avenue of the Americas
JAPR-1995
                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNET/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/668,648 FILING DATE: 13-MAR-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/431,333
FILING DATE: 27-APR-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08431333 Patent No. 5965723
                                                                                                                                                                                                           : TELEFAX: (212)790-9090
: TELEFAX: (212)790-9090
: INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
   LENGTH: 589 amino acids
   TYPE: amino acid
   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KKVIAPRRLPDPQILKSD 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION TELEPHONE: (212)790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 589 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 64.6
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-429-998-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                     FILING DATE: 27 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POPOLOGY:
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Matches

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RESULT 12

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNET/AGENT INFORMATION:
                                                                                                                                                                                                                                                                ZIP: 100,50
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
Anneraling SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08431333;
Patent No. 5965723
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: BPITHELINS: NC
TITLE OF INVENTION: MODILATING PRO
TITLE OF INVENTION: MODILATING PRO
TITLE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     346 EKAPAHLSLPDPQALKRD 363
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COMPUTER: IBM PC compatible
                                                                                                                                                               Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.8%;
nilarity 55.6%;
Conservative
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TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 593 amino acids
amino acid
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohan
APPLICANT: Plowman, Greg
TITLE OF INVENTION: EPIT
TITLE OF INVENTION: MODU
TITLE OF INVENTION: MODU
TITLE OF SOUTHORES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-429-998-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
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Best Local Similarity
Matches 10; Conserve
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                                                                                                                                                                               1155
                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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                                                                             FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)...(19)
OTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody.
US-08-991-862-6
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/07668648
Patent No. 5416192
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowah, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 593;
                                                                                                                                                                                                                      45.8%; Score 44; DB 4; Length 19; 55.6%; Pred. No. 0.45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                              7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,648
FILING DATE: 19910819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/POCKET NUMBER: 5624
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08429998
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1 Similarity 55.6%;
10; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 593 amino acids
AMINO ACID
                                                                                                                                                                                                                                                            10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                            TYPE: PRT
ORGANISM: Human granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: EP
TITLE OF INVENTION: MOI
NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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Matches 10; Conserv
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New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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STREET: 11
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US-08-429-998-4
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STATE:
    SEQ ID NO 6
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Gregory D. EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
Gregory D. EPITHELINS: NOVEL CYSTEINE-RICH GROWTH MODULATING PROTEINS
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                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/429,998
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB 2;
Pred. No. 23;
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1155 Avenue of the Americas
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TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFRENCE: 29996.488/P01.A
CURRENT APPLICATION NUMBER: US/08/991,862
CURRENT FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/863,862
EARLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 17
LENGTH: 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                    45.8%; Score 44; DB 2; Length 593;
55.6%; Pred. No. 23;
tive 1; Mismatches 7; Indels
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APPLICATION NUMBER: US/08/431,333
FILING DATE: 27-APR-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MR-1991
ATTORNET/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/08991862 Patent No. 6309826
                                                                                                                                      NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,972
REFERENCE/DOCKET NUMBER: 5624
TELEPHONE: (212)790-9090
TELEPHONE: (212)790-9741
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: amino acid
TOPOLOGY: linear
WOLECULE TYPE: protein
US-08-431-333-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 EKAPAHLSLPDPQALKRD 363
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Best Local Similarity 55.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 55.6%
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Human GP88 cDNA
US-08-991-862-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-08-991-862-17
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Search completed: July 8, 2003, 16:30:16 Job time: 13.6923 secs

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GenCore version 5.1.6
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 protein search, using sw model OM protein July 8, 2003, 16:24:26; Search time 18.5128 Seconds (without alignments) 119.483 Million cell updates/sec Run on:

US-09-824-647-3 96

Title: Perfect score: Sequence:

1 KKVIAPRRLPDPQILKSDT 19 Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

445758 seqs, 116419773 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published_Applications_AA:

6/ptodata/2/pubpaa/US06_NEW_PUB.pep: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:

/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

ptodata/2/pubpaa/US10_NEW_PUB.pep: ptodata/2/pubpaa/US10_PUBCOMB.pep: ptodata/2/pubpaa/US60_NEW_PUB.pep: /cgn2_6/ptcdata/2/pubpaa/US08_NEW_PUB.pep:*/cgn2_6/ptcdata/2/pubpaa/US08_PUBCOMB.pep:*/cgn2_6/ptcdata/2/pubpaa/US09_NEW_PUB.pep:*/cgn2_6/ptcdata/2/pubpaa/US09_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:

SUMMARIES

	Description	Sequence 3, Appli	-	Ή,	'n	ω,	4		2;	Sequence 2, Appli	Sequence 2, Appl1	11,	~	9	Sequence 6, Appli	9	Sequence 6, Appl1	Sequence 6, Appli	Sequence 11112, A	Sequence 17, Appl
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	ΙD	US-09-824-647-3	US-10-218-509-3	US-10-281-160-3	US-09-813-156-3	US-09-824-807-3	US-09-824-647-2	US-10-218-509-2	US-10-281-160-2	US-09-813-156-2	US-09-824-807-2	US-09-800-971-11	US-10-226-844-1	US-09-824-647-6	US-10-218-509-6	US-10-281-160-6	US-09-813-156-6	US-09-824-807-6	US-10-156-761-11112	US-09-824-647-17
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	Query Match Length DB	19	19	19	19	19	589	589	589	589	589	92	824	19	19	19	19	19	319	593
æ	Query Match	100.0	100:0	100.0	100.0	100.0	92.7	92.7	92.7	92.7	92.7	49.0	47.9	45.8	45.8	45.8	45.8	45.8	45.8	45.8
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Sequence 3, Application US/10218509 Publication No. US20030092661A1 GENERAL INFORMATION:

US-10-218-509-3

RESULT 2

Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 11, Appl Sequence 13, Appl Sequence 514, Appl Sequence 6120, Appl Sequence 46, Appl Sequence 47, Appl Sequence 4, Appl Sequence 178, Appl Sequence 178, Appl Sequence 2, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 17, Appl Sequence 64, Appl Sequence 64, Appl
9 US-10-218-509-17 9 US-10-281-160-17 10 US-09-813-156-17 10 US-09-825-301-416 10 US-09-925-301-416 10 US-09-925-301-416 10 US-09-918-626-13 10 US-09-738-626-5837 9 US-09-738-626-5837 9 US-09-738-626-5837 9 US-09-738-626-5837 9 US-09-31-34-4 10 US-09-948-369-4 10 US-09-948-369-14 10 US-09-948-369-14 10 US-09-948-369-16 12 US-10-34-455-17 10 US-09-948-369-16 12 US-10-34-849-2 12 US-10-34-849-2 13 US-10-34-849-2 14 US-09-948-369-16 15 US-10-34-849-2 16 US-09-948-369-16 17 US-10-34-849-2 18 US-10-166-886-19 18 US-10-166-886-19 18 US-09-883-166-19
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ALIGNMENTS

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Gaps
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SETTERO.

TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
TITLE OF INVENTION: 88 KDA TUMORISE SOURCE
CURRENT APPLICATION NUMBER: US/09/824,647
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/863,862
PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1)..(19)
OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the OTHER INFORMATION: antisera against the GP88 used in the OTHER INFORMATION: immunoaffinity step.
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100.0%; Score 96; DB 9;
Best Local Similarity 100.0%; Pred. No. 8.9e-09;
Matches 19; Conservative 0; Mismatches 0;
Sequence 3, Application US/09824647 Publication No. US20020183270A1 GENERAL INFORMATION:
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NAME/KEY: PEPTIDE
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LENGTH: 19
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Sequence 3, Application US/09824807

Patent No. US20020094966A1

GENERAL INFORMATION:

APPLICANT: Serrero, Ginette

TITLE OF INVENTION:

FILE REPERENCE: 29996.488 FDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS

FILE REPERENCE: 29996.488 FDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS

FURNER APPLICATION UNMBER: 08/991,862

PRIOR FILING DATE: 1997-12-16

PRIOR FILING DATE: 1997-05-23

FRIOR PRILING DATE: 1997-05-23

WHIGHER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver: 2.0
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                                                    TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
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100.0%; Pred. No. 8.9e-09;
tive 0; Mismatches 0;
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                                                                      FILE REFERENCE: 2996.488/P001.A
CURRENT APPLICATION NUMBER: US/09/813,156
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1997-12-16
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENT NOY. 2.0
SOFTWARE: PATENT NOY. 2.0
SERIOR DIO 3
SEQ ID NO 3
SEQ ID NO 3
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; Sequence 2, Application US/09824647
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Best Local Similarity 100.
Matches 19; Conservative
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Best Local Similarity
Matches 19; Conserva
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APPLICANT: Seriero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REPERENCE: 2996.488/P001-A
CURRENT APPLICANION NUMBER: US/10/218,509
CURRENT FILING DATE: 2002-08-15
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3: 17
LENGTH: 19
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APPLICANT: Serrero, Ginette
TITLE OF INFORMATION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 2996/448/F001-8
CURRENT APPLICATION NUMBER: US/10/281,160
CURRENT FILING DATE: 2002-10-28
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LOCATION: (1)..(19)
OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the
OTHER INFORMATION: antisera against the GP88 used in the
OTHER INFORMATION: immunoaffinity step.
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OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the OTHER INFORMATION: antisera against the GP88 used in the OTHER INFORMATION: immunoaffinity step.
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Best Local Similarity 100.0%; Pred. No. 8.9e-09;
Matches 19; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 8.9e-09;
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PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
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; Patent No. US20020061859A1
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Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                              ORGANISM: mouse granulin
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US-09-813-156-3
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NUMBER OF SEQ ID NOS: 17
                      SOFTWARE: PatentIn Ver.
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US-09-824-807-2
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LENGIH: 589
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                                             SEQ ID NO 2
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Eublication No. US20030092661A1
GENERAL INFORMATION:
APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REPERENCE: 2996.488/P001.A
CURRENT APPLICATION NUMBER: US/10/218,509
CURRENT FILING DATE: 2002-08-15
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GENERAL INFORMATION:
APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REPERENCE: 2996.488/P001-A
CURRENT APPLICATION UNDBER: US/10/281,160
CURRENT FILING DATE: 2002-10-28
                                         APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 2996.488/P001-A
CURRENT APPLICATION NUMBER: US/09/824,647
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: ENRIER APPLICATION NUMBER: 08/991,862
PRIOR PELING DATE: EARLIER FILING DATE: 1998-08-17
PRIOR PELING DATE: EARLIER ERLIER APPLICATION NUMBER: 08/863,862
PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23
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Pred. No. 6.1e-06;
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Pred. No. 6
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PRIOR FILING DATE: 1998-08-17
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PRIOR FILING DATE: 1998-08-17
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PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mouse epithelin/granulin
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Best Local Similarity 94.7%;
Matches 18; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                   92.7%;
US20020183270A1
                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 589
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 92.77
Best Local Similarity 94.77
Matches 18; Conservative
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LENGTH: 589
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Sequence 2, Application US/09813156
Patent No. US20020061859A1
GENERAL INFORMATION:
APPLICATION:
APPLICATION:
TILLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/09/813,156
CURRENT FILING DATE: 1997-12-16
PRIOR PLICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1997-12-16
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VOE: 2.0
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Serrero, Ginette TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS FILE REFERENCE: 29996.488/P001-A CURRENT APPLICATION NUMBER: US/09/824,807 CURRENT FILING DATE: 2001-04-04
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                                                                                     Length 589;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 89; DB 10;
Pred. No. 6.1e-06;
0; Mismatches 1;
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Pred. No. 6.1e-06;
0; Mismatches 1;
                                                                                     Query Match 92.7%; Score 89; DB 9; Best Local Similarity 94.7%; Pred. No. 6.1e-06; Matches 18; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1997-12-16
PRIOR FILING DATE: 1997-62-23
NUMBER OF SEQ ID NOS: 17
SOGTWARE: Patentin Ver. 2.0
SEQ ID NO ED NOS: 17
LENGTH: 589
TYPE: PRT; ORGANISM: Mouse epithelin/granulin
US-10-281-160-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Mouse epithelin/granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mouse epithelin/granulin
US-09-824-807-2
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Patent No. US20020094966A1
                                                                                                                                                                                                            1 KKVIAPRRLPDPQILKSDT 19
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Best Local Similarity 94.7%;
Matches 18; Conservative
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Best Local Similarity 94.7%;
Matches 18; Conservative
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Wed Jul

RESULT 11 US-09-800-971-11

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Sequence 6, Application US/10218509
Publication No. US20030092661A1
GENERAL INFORMATION:
APPLICANT: Serreto, Ginette
TITLE OF INVENTION:
RESTERENCE: 29996.488/P001-A
FILE REPERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: 08/991,862
PRIOR PLING DATE: 1099-08-15
PRIOR PLING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATCHIN VOIT: 2.0
                                                                    APPLICAMT: Serrero. Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILLE REFERENCE: 2999-488/P001-A
CURRENT APPLICATION NUMBER: US/09/824,647
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-08-17
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17
PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23
NUMBER OF SEG'ID NOS: 17
SOFTWARE: PATÈNTING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KET: PEPTIDE
LOCATION: (1). (12)
COTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (1)...(19)
; OTHER INFORMATION: Internal peptide of human GP88 used to develop
; OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
US-10-218-509-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB 9;
Pred. No. 1.4;
1; Mismatches
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Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
Sequence 6, Application US/09824647 Publication No. US20020183270A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 55.6%;
Matches 10; Conservative
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Best Local Similarity 55.69
Matches 10; Conservative
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ORGANISM: Human granulin
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Publication No. US20030113764A1

GENERAL INFORMATION:
APPLICANT: Bodary, Sarah C.
APPLICANT: Bodary, Sarah C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMORS
FILE REFERENCE: P1773R1
CURRENT APPLICATION NUMBER: US/10/226,844
CURRENT APPLICATION NUMBER: US/09/627,202
PRIOR APPLICATION NUMBER: US/09/627,202
PRIOR APPLICATION NUMBER: US 60/146,217
PRIOR FILING DATE: 1999-07-28

NUMBER: OF SEQ ID NOS: 22
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TITLE OF INVENTION: 16835, A NOVEL HUMAN PHOSPHOLIPASE C
TITLE OF INVENTION: 16835, A NOVEL HUMAN PHOSPHOLIPASE C
TITLE OF INVENTION: 16835, A NOVEL HUMAN PHOSPHOLIPASE C
TITLE OF INVENTION: 10448-023001
CURRENT FILING DATE: 2001-03-06
CURRENT FILING DATE: 2001-03-06
PRIOR PPLICATION NUMBER: 60/187,453
PRIOR PPLICATION NUMBER: 60/189,032
PRIOR FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 46; DB 9; Length 824;
Pred. No. 55;
5; Mismatches 3; Indels
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Pred. No. 3;
3; Mismatches 6
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47.9%; Score 46;
Best Local Similarity 43.8%; Pred. No. 3
Matches 7; Conservative 6; Mismatch
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                                                                                                                                                                                             Sequence 11, Application US/09800971
Patent No. US20020098577A1
GENERAL INFORMATION:
                        2 KVIAPRRLPDPQILKSDT 19
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Best Local Similarity 50.0%;
Matches 9; Conservative
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ORGANISM: Homo sapien
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Gaps

RESULT 13 US-09-824-647-6

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US-10-226-844-1

SEQ ID NO 1

0; Gaps

Score 44; DB 9; Length 19; Pred. No. 1.4; 1; Mismatches 7; Indels

Query Match Best Local Similarity 55.6%; Matches 10; Conservative Search completed: July 8, 2003, 16:31:39 Job time : 19.5128 secs

Q D us-09-824-647-3.rpr

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

8, 2003, 16:19:45; Search time 19.2436 Seconds (without alignments) 94.918 Million cell updates/sec July Run on:

1 KKVIAPRRLPDPQILKSDT 19 US-09-824-647-3 96 Title: Perfect score: Sequence:

Scoring table:

283224 seqs, 96134422 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283224

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:* pir3:* pir4:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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Description	epithelin/dranulin	epithelin/granulin	UDPglucose 4-epime	beta-ketoacyl redu	granulin precursor	late embryogenesis	hypothetical prote	hypothetical prote	₩.	hypothetical prote		ᆢ	alpha-amylase (EC	hypothetical prote	thra bifunctional	aspartokinase I-ho	aspartokinase I, h	aspartokinase I/ho	probable dnaB prot	hypothetical prote	conserved hypothet	apical membrane an	apical membrane an	apical membrane an	UDP-N-acetylpyruvo	hypothetical prote	alcohol dehydrogen	probable exported	qlutamate-tRNA 11q
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D	C38128	B38128	F81317	F83221	GYHU	T07099	T00150	H87710	S56142	T01619	S74911	D70987	JC5132	D70709	DEECK	B90629	B85480	AC0502	B70914	S28721	E82973	D44986	B44986	A32499	G82541	T51200	D69583	AH1053	C70146
DB	2	~	~	~	Н	~	~	7	~	N	7	7	7	~	-1	~	~	~	'n	ď	~	~	7	7	~	~	H	7	~
Length	589	589	328	256	593	174	223	344	260	753	244	280	256	266	820	820	820	820	874	1650	450	622	622	622	351	368	378	462	490
Query Match	100.0	64.6	50.0	46.4	45.8	44.8	44.8	44.8	44.8	44.8	43.8	43.8	43.8	43.8	43.8	4.3.8	43.8	43.8	43.8	43.8	43.2	43.2	43.2	43.2	42.7	42.7	42.7	42.7	42.7
Score	96	62	48	44.5	44	43	43	43	43	43	. 42	42	42	42	42	42	42	42	. 42	42	41.5	41.5	41.5	41.5	41	41	41	41	41
Result No.	-	7	e	❖	Ŋ	•	7	80	ď	10	11	. 12	. 13	14	15	. 16	17	18	19	. 50	21	22	23	24	. 52	56	27	28	53

A;Molecule_type: protein A;Residues: 18-19,'X',21-25,'X',27-29,'XX',32;'XXX',119-127;152-154,'DXK',158-16:

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Gaps

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Length 589;

Query Match
100.0%; Score 96; DB 2; Best Local Similarity, 100.0%; Pred. No. 1.2e-07; Matches 19; Conservative 0; Mismatches 0;

C; Superfamily: granulin

preliminary

A; Accession: A46705

Q Q

RESULT B38128

D-xylose transport hypothetical prote probable b2IP prot	cell division prot probable membrane hypothetical prote	repirection associ probable dTDP-4-ke protein FINI9-5 [1 outer membrane pro outer membrane pro	outer membrane pro outer membrane pro outer membrane pro probable hydrolase cyclin D3 - rat	-
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AG3527 T04980 D96563	A81741 S50293 AF3219	T10115 T46530 F96668 162394 162391	162387 162389 162393 F70790 JC4012	
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512 750 798	794 025 114	195 195 224 240	44 44 44 64 93	
	-		00000	
	-	41.7 41.7 41.7 41.7		
42.7	-			

ALIGNMENTS

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Gross-references: GB:X62321; NID:950851; PIDN:CAA44197.1; PID:950852
Baba, T.; Nemoto, H.; Watanabe, K.; Arai, Y.; Gerton, G.L.
Baba, T.; Nemoto, H.; Watanabe, K.; Arai, Y.; Gerton, G.L.
Baba, T.; Nemoto, H.; Watanabe, K.; Arai, Y.; Gerton, G.L.
Filtle: Exon/Antron organization of the gene encoding the mouse epithelin/granu.
Reference number: S32503; MUID:93245991; PMID:8482392
                                                                              C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 10-Jul-1992 fsequence_revision 10-Jul-1992 ftext_change 20-Aug-1999
C; Accession: C38128; S32503; 149468; A46705
R; Plowman, G.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Todi R; Plowman, G.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Todi A; Etol.; Chem. 267, 13073-13078, 1992
A; Itle: The epithelin precursor encodes two proteins with opposing activities or A; Reference number: A38128; MUID:92317004; PMID:1618805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;MOLECULE type: DNA
A;Residues: 18-349,'L',351-589 <BAB>
A;Residues: 18-34, H.B. .
Mol. Reprod. Dev. 34, 233-243, 1993
A;Title: Acrogranin, an acrosomal cysteine-rich glycoprotein, is the precusor of
A;Reference number: 148141; MUID:93228994; PMID:8471244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . Biol. Chem. 268, 10863-10869, 1993
:Title: Purification of an autocrine growth factor homologous with mouse epithe.
:Reference number: A46705; MOID:93266526; PMID:8496151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    esidues: 1-250,'L',252-253,'V',255-349,'L',351-401,'SA',404-589 <RES> ross-references: GB:MG6736; NID:g191766; PIDN:AAA37191.1; PID:g191767 hou, J.; Gao, G.; Crabb, J.W.; Serrero, G. Biol. Chem. 268, 10863-10869, 1993
                        N; Alternate names: acrogranin; PC-cell-derived growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: preliminary; translated from GB/EMBL/DDBJ
- mouse
epithelin/granulin precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: mRNA
Residues: 1-589 <PLO>
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Gaps

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Indels

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C; Accession: F83221
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Ature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: epithelin
N;Contains: granulin A; granulin B; granulin C; granulin D; granulin B; granulin F;
C;Species: Homo saptens (man)
C;Species: Jo-Sep-1992 #sequence_revision 03-May-1996 #text_change 08-Dec-2000
C;Accession: JC1284; A38128, A38128; A36698; B36698; C36698; B36698; A56873
R;Bhandari, V.; Bateman, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-593 <BHA>
R; Residues: 0.593 <BHA>
B; Residues: 0.593 <BHA>
A; Residues: 0.593 <BHA>
A; Rithe: The epithelin precursor encodes two proteins with opposing activities on € A; Reference number: A38128; MUID:92317004; PMID:1618805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: GB:X62320; NID:g31192; PIDN:CAA44196.1; PID:g31193; Bhandari, V.; Palfree, R.G.E.; Bateman, A. croc. Natl. Acad. Sci. U.S.A. 89, 1715-1719, 1992; Title: Isolation and sequence of the granulin precursor cDNA from human bone marx Reference number: A38118; MUID:92179253; PMID:1542665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Residues: 1-406,'R',408-433,'G',435-453,'G',455-459,'Q',461-546,'A',548-566,'R',5
Cross-references: GB:M75161; NID:9183612; PIDN:AAA58617_1; PID:9183613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: rhlG; PA3387
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
                                                                                                                                                                                                                                                                                                                                                     oeta-ketoacyl reductase PA3387 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB: AE004760; GB: AE004091; NID: 99949520; PIDN: AAG06775.1;
                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 188, 57-63, 1992
A; Title: Structure and chromosomal location of the human granulin gene.
A; Reference number: JC1284; MUID:93038704; PMID:1417868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E, D.; Bennett, H.; Lazure, C.; Solomon, Commun. 173, 1161-1168, 1990
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        9
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Pred. No. 12;
3; Mismatches
        Mismatches
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280 KVELAPRRAGDPSVLISD 297
        ä
                                                                            1 KKVIAPRRLPDPQILKSD 18
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ilarity 42.38;
Conservative
        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-256 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -593 <PLO>
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Molecule type: DNA
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Best Local Simi
Matches 11;
        10;
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        Matches
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P81317
UDPGlucose 4-epimerase (EC 5.1.3.2) Cjl131c [imported] - Campylobacter jejuni (strain NC c; Species: Campylobacter jejuni
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C; Accession: P81317
R; Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C; W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A; Tille: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A; Reference number: A81250; MUID:20150912; PMID:10688204
A; Residues: Prellminary
A; Restdues: 1-328 <-Park
A; Restdues: 1-328 <-Park
A; Restdues: 1-328 <-Park
A; Cross-references: GB:AL139077; GB:AL111168; NID:g6968444; PIDN:CAB73386.1; PID:g696856
A; Experimental source: serotype 02, strain NCTC 11168
C; Genetics:
A; Genetics:

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A; Title: Granulins, a novel class of peptide from leukocytes.
A; Reference number: A36698; MUID:91097544; PMID:2268320
A; Accession: E36698
A; Molecule type: protein
A; Residues: 279-307, 582, 130-324, 'T', 326, 'X', 328, 'Q' < BAT>
A; Molecule type: protein
A; Residues: 279-307, 582, 1993
A; Title: The complementary deoxyribonucleic acid sequence, tissue distribution, and cell
A; Reference number: 153272; MUID:94062640; PMID:8243292
A; Reference number: 153272
A; Reference number: 153272
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-200, 'S', 203-388, 'M', 390-589 < RES>
A; Cross-references: GB M97750; NID:9204223; PIDN:AAA16903.1; PID:9204224
C; Superfamily: granulin
epithelin/granulin precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 20-Aug-1999
C;Accession: B38128; A36199; B36619; B36699; I53272
R;Plowman, G.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Todaro, G.J.
A; Biol. Chem. 267, 13073-13078, 1992
A;Title: The epithelin precursor encodes two proteins with opposing activities on epithe
A;Reference number: A38128; MUID:92317004; PMID:1618805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title: Epithelins 1 and 2: isolation and characterization of two cysteine-rich growth-Reference number: A36199; MUID:91045907; PMID:2236009
Accession: A36199
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                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-589 <PLO>
A; Cross-references: GB: X62322; NID: 956108; PIDN: CAA44198.1; PID: 956109
A; Cross-references: GB: X62322; NID: 956108; C: ? Todaro, G.J.; Plowman, G.D.
Proc. Natl. Acad. Sci. U.S.A. 87, 7912-7916, 1990
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Pred. No. 4.2;
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Pred. No. 0.043;
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Best Local Similarity 72.2%;
Matches 13; Conservative
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55.6%;
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Residues: 280-300 <SHO>
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Residues: 205-226 <SH2>
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Best Local Similarity
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R;Kaneko, J; Kimura, Y;; Kawakami, Y.; Tomita, T.; Kamio, Y.
Biosci. Biotechnol. Biochem. 61, 1960-1962, 1997
A;Title: Panton-Valentine leukocidin genes in a phage-like particle isolated fro A;Reference number: 214119; MUID:98067870; PMID:9404084
A;Accession: T00150
A;Status: translated from GB/EMBL/DDBJ
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C; Accession: H87710

W.C; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidel
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fras
Proc. Natl. Acad. Scl. US.A. 98, 4136-4141, 2001
A; Title: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Molecule type: DNA
A:Residues: 1-223 <KAN>
A;Cross-references: EMBL:AB009866; NID:d1204727; PIDN:BAA31890.1; PID:d1032851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Species: Staphylococcus aureus phage phi PVL
C.Date: 23-Apr.1999 #sequence_revision 23-Apr.1999 #text_change 11-May-2000
C.Accession: T00150
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C;Date: 20-Apr-2001 *sequence_revision 20-Apr-2001 *text_change 10-May-2001
                                                                                                                                                                                                     Length 174率
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hypothetical protein CC3722 [imported] - Caulobacter crescentus
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                                                                                                                                                                                                                                                               4; Indels
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Pred. No. 13;
5; Mismatches
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Pred. No. 18;
1; Mismatches
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C;Superfamily: phosphoglycerate dehydrogenase
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Best Local Similarity 57.1%;
Matches 8; Conservative
                                                                                                                                                                                                     / Match 184.8%;
Local Similarity 47.1%;
nes 8; Conservative
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141 PNNLPNPSISNSDT 154
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                                                                                        A; Molecule type: mRNA
A; Residues: 1-138, 'RRV' <VA2>
A; Cross-references: EMBL: Z46654
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KVIVTRKLPDP 33
A; Reference number: S49580
A; Accession: S49580
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Best Local Similarity
Matches 8; Conserv
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A;Molecule type: DNA
A;Residues: 1-344 <STO>
                                                         A; Status: preliminary
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Matches
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A;Introns: 46/3; 88/3; 117/1; 154/3; 200/1; 236/3; 279/1; 311/3; 393/3; 471/3; 548/3
C;Superfamily: granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A)Cross-references: EMBL:246654; PIDN:CAA86613.1
A)Experimental source: strain Marmande; Meloidogyne incognita-induced root knot (8 xvan der Eycken, W.; de Almeida Engler, J.; Inze, D.; van Montagu, M.; Gheysen, submitted to the EMBL Data Library, November 1994
A)Description: A molecular study of Meloidogyne incognita-induced feeding sites.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Residues: 442-46, XXTSS',456-458, 'DG' <BA4>
Rardana, A.; Bagshave, K.D.; Coles, B.; Read, D.; Taylor, M.
r. J. Cancer 67, 686-692, 1993
Title: Characterisation of UGP and its relationship with beta-core fragment.
Reference number: A56873; MUID:93229246; PMID:8471426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Iycopersicon esculentum (tomato)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 01-Dec-2000
C;Accession: T07099; S49580
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                                                                                  A;Wolecule type: protein
A;Residues: 281-336 <BAT>
A;Note: this protein was purified and characterized as granulin
A;Accession: B36698
                                                                                                                                                                                            A;Wolecule type: protein
A;Residues: 206-218,'H',220-233 <BA2>
A;Note: this protein was purified and characterized as granulin
A;Accession: C36698
                                                                                                                                                                                                                                                                                                                   Molecule type: protein
Residues: 364-367, X',369-385, H',387-396 <BA3>
Note: this protein was purified and characterized as granulin Accession: D36698
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      tle: Granulins, a novel class of peptide from leukocytes.
ference number: A36698; MUID:91097544; PMID:2268320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: sequence extracted from NCBI backbone (NCBIP:129524)
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1-17/Domain: signal sequence #status predicted <$IG>
18-593/Product: granullin #status predicted <WAT>
18-593/Product: progranulin #status predicted <PRO>
18-694/Product: paragranulin #status experimental <PGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;58-113/Product: granulin G *status predicted <GRG>F;121-179/Product: granulin F *status predicted <GRF>F;266-261/Product: granulin B *status experimental <GRB>F;261-336/Product: granulin A *status experimental <GRA>F;
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F:442-496/Product: granulin D *status predicted <GRD>
F:518-573/Product: granulin E *status predicted <GRE>
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38;
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A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Molecule type: protein
A:Residues: 281-283,'X',285-289,'S',291-295 <KAR>
A:Experimental source: urine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ed. No. 38;
Mismatches
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submitted to the EMBL Data Library, August 1997
A; Reference number: 215918
A; Accession: T07099
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GDB:136006; OMIM:138945
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8est Local Similarity 55.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: protein
Residues: 442-446,'XDTS
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                                                            Accession: A36698
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A; Map position: 2
A; Introns: 78/2; 606/1; 705/1; 737/3
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70.0%;
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Best Local Similarity 58.8%;
Matches 10; (Conservative
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Best Local Similarity 63.0v
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148 LPQPQVIKIDT 158
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                                                                                             C;Genetics:
A;Gene: At2g18910; F19F24.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Synechocystis sp. A; Variety: PCC 6803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 PRRLPDPQIL 15
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Best Local Similarity
Matches 7; Conserv
A; Molecule type: DNA
A; Residues: 1-753 <STO>
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NyAlternate names: hypothetical protein F19F24.11
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 02-Feb-2001
C; Accession: T01619; B84570
R; Rounalsty, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul submitted to the EMBL Data Library, April 1998 II BAC F19F24 genomic sequence.
A; Recession: T01619
A; Reference number: 214153
A; Accession: T01619
A; Status: translated from GB/EMBL/DDBJ
A; Residues: 1-753 < ROUS
A; Residues: 1-753 < ROUS
A; Residues: 1-753 < ROUS
A; Experimental source: cultivar Columbia
A; Experimental source: cultivar Columbia
B; Lin, X.; Raul, S.; Rounaley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. A; Reference and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84700; MUDD:20083487; PMID:10617197
A; Reference number: A8450; MUDD:20083487; PMID:10617197
                                              ;Species: Schizosaccharomyces pombe;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 10-Dec-1999;Accession: S56142; A56106; T38697
;Parlati, F.; Dignard, D.; Bergeron, J.J.M.; Thomas, D.Y.
MBO J. 14, 3064-3072, 1995
;Title: The calnexin homologue cnx1(+) in Schizosaccharomyces pombe, is an essential generation number: S56142; MUID:95347333; PMID:7621821
                                                                                                                                                                                                                                                                                                                                           Residues: 1.560 <PAR>
(Cross -references: EMB:M98799; NID:g437733; PIDN:AAA79757.1; PID:g437734
(Cross -references: EMB:M98799; NID:g437733; PIDN:AAA79757.1; PID:g437734
(Januaripour, M.; Rokeach, L.)
(Biol. Chem. 270; 4845-4853, 1995
(Jitle: The Schizosaccharomyces pombe homologue of the chaperone calnexin is essential Reference number: A56106; MUID:95181485; PMID:7876257
- fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: 21805
A; Accession: T38697
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-560 <BRO>
A; Cross references: EMBL:299568; PIDN:CAB16741.1; GSPDB:GN00066; SPDB:SPAC3C7.11c
A; Experimental source: strain 972h-; cosmid c3c7
C; Genetics:
A; Gene: SPDB:SPAC3C7.11c
A; Map position: 1
A; Map position: 1
C; Superfamily: calnexin
C; Superfamily: calnexin
C; Reywords: calcium binding
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                        Alternate names: calnexin homolog cnx1
precursor cnx1
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50.0%;
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274 APRMIPDPDAVKPE 287
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Matches 7; Conserv
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C;Accession: S;4911
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Tamada, M.; J DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gorć; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroy Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete ge A; Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:D90909; GB:AB001339; NID:91652844; PIDN:BAA17872.1; PID:d1
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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A; Cross-references: GB: AE002093; NID: 93004565; PIDN: AAC09038.1; GSPDB: GN00139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-0ct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein sll1950 - Synechocystis sp. (strain PCC 6803)
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A; Accession: S74911
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Pred. No. 29;
2; Mismatches
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                                                                                                                                                                         ore 43; DB 2 ed. No. 73; Mismatches
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Pred. No. 34;
2; Mismatches
                                                                                                                                                                            Score 43;
Pred. No.
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A; Rose, D. J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A; Rose, D. J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A; Title: The complete genome sequence of Escherichia coli R-12.

A; Reference number: A64720; MUID:97426617; PMID:9278503

A; Reference number: A64720; MUID:97426617; PMID:9278503

A; Recession: B64720

A; Status: nucleic acid sequence not shown; translation not shown

A; Residues: 1-820 (BLAT>

A; Residues: 1-820 (BLAT>
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A; Residues: 1-10, 'L', 12-229, 'N', 231-374, 'L', 376-392, 'A', 394-405, 'L', 407-552, 'N', 5
A; Cross-references: GB:J01706; EMBL:V00360; NID:g147977; PIDN:AAA83914.1; PID:g14
A; Note: Lits sequence has been revised in reference A00671
B; Stbilli, L; Le Bras, G; Cossart, P; Chalvignac, M.A.; Le Bras, G.; Brilley, I
B; Stbilli, L; Le Bras, G; Cossart, P; Chalvignac, M.A.; Le Bras, G.; Brilley, I
B; Stbilli, L; Le Bras, G; Cossart, P; Chalvignac, M.A.; Le Bras, G.; Brilley, I
B; Stbilli, L; Le Bras, G; Cossart, P; Chalvignac, M.A.; Le Bras, G.; Brilley, I
A; Steference number: A14560; MuID:80043179; PMID:387092
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A; Residues: 1-229, 'N', 231-374, 'L', 376-392, 'A', 394-405, 'L', 407-552, 'N', 554-606, 'I'
A; Residues: 1-229, 'N', 231-374, 'L', 376-392, 'A', 394-405, 'L', 407-552, 'N', 554-606, 'I'
R; Katinka, M.; Cossart, P.; Sibilli, L.; Saint-Girons, I.; Chalvignac, M.A.; Le F
R; Katinka, M.; Cossart, P.; Sibilli, L.; Saint-Girons, I.; Chalvignac, M.A.; Le F
R; Katinka, M.; Cossart, P.; Sibilli, L.; Saint-Girons, I.; Chalvignac, M.A.; Le F
R; Katinka, M.; Cossart, P.; Sibilli, L.; Saint-Girons, S.; Saint-Girons, S
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R. Cossart, P.; Ratinka, M.; Yantv, M.
Mol. Gen. Genet. 175, 39-44, 1979
A. Title: Construction and expression of a hybrid plasmid containing the Eschericl
A. Reference number: 157719; MUID:80077291; PMID:390305
A. Accession: 157719
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A,Residues: 1-820 <BURS.
A,Gross-references; EMBL:U14003; NID:g1263172; PIDN:AAA97301.1; PID:g537245
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, August 15
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A;Residues: 51-112, E',114-129 <SIB>
A;Residues: 51-112, E',114-129 <SIB>
A;Residues: 51-112, E', Magai, H.; Nagai, T.; Ishihama, A.; Fujita, N.; Isono, K.;
Submitted to the EMBL Data Library, December 1992
A;Description: Systematic sequencing of the Escherichia coli genome: analysis of
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A;Residues: 1-10,'L',12-229,'N',231-374,'L',376-392,'A',394-405,'L',407-552,'N',!
A;Cross-references: EMBL:D10483; NID:g216434; PIDN:BAA01286.1; PID:g216435
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A;Title: Initiation, pausing, and termination of transcription in the threonine of A;Reference number: 155222; MUID:82142573; PMID:6277952
A;Accession: 169970
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J. Wol. Biol. 183, 529-541, 1985
A;Title: Identification and characterization of mutants affecting transcription
G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unpublished results, cited by Zakin, M.M., Duchange, N., Ferrara, P., and Cohen,
A;Reference number: A00671
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A.Residues: 553-586,'IT' <COS2>
A.Cross-references: GB:M10644; NID:g147982; PIDN:AAA24671.1; PID:g147983
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             F.R.; Plunkett III,
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A; Residues: 1-10 <GAR>
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N;Alternate names: aspartokinase I / homoserine dehydrogenase I; protein f132
N;Contains: aspartate kinase (EC 2.7.2.4) I [validated]; homoserine dehydrogenase (EC
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C;Date: 31-Dec-1980 #sequence_revision 10-Oct-1997 #text_change 01-Mar-2002
C;Accession: B64720; S56629; A00671; A15659; A14560; S40531; I57719; I69970; I73480
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C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: D70709
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Pred. No. 75;
2; Mismatches
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76;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: strain ATCC33909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alternate names: glycogenase; Species: Sulfolobus acidocaldarius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KKVIAPRRLPDPQILKSD 18
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Best Local Similarity 55.6%;
Matches 10; Conservative
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RVVAPHRLTDPK 483
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PYRVPDPQIM 264
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7; Conserve
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A; Description: as homoserine dehydrogenase catalyzes the reduction by NADH of aspartate A; Pathway: glycine metabolism; serine metabolism; threonine biosynthesis C; Superfamily: thrA bifunctional enzyme; aspartate kinase homology; homoserine dehydroge C; Superfamily: thrA bifunctional enzyme; aspartate kinase homology; homoserine dehydrogenase; F;1-460/Domain: aspartate kinase homology KI>>
F;463-719/Domain: homoserine dehydrogenase homology KBD>
F;467-495/Region: beta-alpha-beta NAD(P) nucleotide-binding fold
                                                                                                                                                                                                                                                                                                                                                                                       A; Description: as aspartate kinase, catalyzes the phosphorylation by ATP of aspartate A; Pathway: aspartate metabolism A; Note: regulated allosterically by L-threonine C; Function: <HON>
                                                                                                                         A; Molecule type: DNA
A; Residues: 1-10 <LIN>
A; Cross-references: GB:M28570; NID:g290476; PIDN:AAA24673.1; PID:g290478
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 42; DB 1; Length 820;
Pred. No. 1.2e+02;
4; Mismatches 1; Indels
A;Reference number: 156399; MUID:85264808; PMID:2410621
A;Accession: 173480
                                                                            A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 43.8%;
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                      A;Gene: thrA; thrAl; thrA2
A;Map position: 0 min
C;Function: <ASP>
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Gaps

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Search completed: July 8, 2003, 16:29:22 Job time: 22.2436 secs

11::11 ::111 237 PRQVPDARLLKS 248 6 PRRLPDPQILKS 17

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

July 8, 2003, 16:16:30; Search time 9.25641 Seconds (without alignments) 85.136 Million cell updates/sec Run on:

US-09-824-647-3 96 1 KKVIAPRRLPDPQILKSDT 19

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result		Query				
No.	Score	Match	Match Length	8	a	Description
г	88	92.7	589	٦	GRN_MOUSE	P28798 mus musculu
7	62	64.6	588	Н	GRN_RAT	P23785 r granulins
Э	46	47.9	824	-	AD08_HUMAN	P78325 homo sapien
4	44.5	46.4	256	Н	RHLG_PSEAE	Q9rpt1 pseudomonas
S	44	45.8	593	Н	GRN_HOMAN	P28799 h granulins
9	43	44.8	260	-	CALX_SCHPO	_
7	42	43.8	514	-	PHLD_MYCTU	Q9xb13 mycobacteri
80	42	43.8	795	Н	PGN_HUMAN	0
6	42	43.8	820	Н	AK1H_ECOLI	l esche
10	42	43.8	867		POL_SRV2	P51517 simian retr
H	42	43.8	874		DNAB_MYCTU	
12	41.5	43.2	622	⊢ 4	AMA1_PLAF8	
13	41.5	43.2	622	~	AMA1_PLAFF	
14	41.5	43.2	622	-	AMA1_PLAFH	
15	41	42.7	490	-	SYE_BORBU	
16	40.5	42.2	643	-	SGT1_ARATH	
17.	40.5	42.2	1025	_	ADA1_YEAST	
18	40	41.7	241	-	OMPA_ESCBL	
19	40	41.7	256	П	6PGL_CHLMU	_
20	40	41.7	257	П	VGLG_BRSVS	O10686 bovine resp
21	40	41.7	293	٦	CGD3_RAT	
22	40	41.7	328	-	GALE_CORDI	P33119 corynebacte
23	40	41.7	330	-	UL16_HSVSA	. 001022 herpesvirus
24	40	41.7	405	Н	Y927_PYRAB	Q9uyv6 pyrococcus
25	40	41.7	503	Н	VL1_HPV26	
56	40	41.7	534	Н	IF2P_SULAC	P95691 sulfolobus
27	40	41.7	819	٦	AK1H_SERMA	P27725 serratia ma
28	40	41.7	830	-	GYRA_BUCAI	P57277 buchnera ap
53	40	41.7	970	-	Y852_HUMAN	
30	39	40.6	126	7	PSAG_CHLRE	P14224 chlamydomon
31	39	40.6	268	-	LPXH_RALSO	Q8y081 ralstonia s
32	39	40.6	329	-	- 1	
33	39	40.6	491	Н	UNC3_CAEEL	Q93705 caenorhabdi

•	p36338 bovine herp	•	_	_	plasmo		P7294 synechocyst	_	_	P30282 mus musculu	P50006 spirulina p	
DRDA AOHAE	UL47 HSVBC	LE14 SOYBN	VL1_HPV31	VL1_HPV58	AMA1_PLAFC	AMA1_PLAFG	EXB2_SYNY3	CGD2_CHICK	CGD3_HUMAN	CGD3_MOUSE	ATPG_SPIPL	٠.
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726	739	152	504	524	622	622	227	291	292	292	310	
9	40.6	40.1	40.1	40.1	40.1	40.1	39.6	39.6	39.6	39.6	39.6	٠,١
90	0.00	38,5	38.5	38.5	38.5	38.5	38	38	38	38	38	
7.0	, c	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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CRN_MOUSE CRN_MOUSE CRN_MOUSE CRN_MOUSE CRN_MOUSE CRN_MOUSE CRN_MOUSE CRN_Created) O1-DEC-1992 (Rel. 30, Last sequence update) O1-OCT-1994 (Rel. 30, Last sequence update) Granulins precursor (Acrogranin) [Contains: Granulin 1; Granulins precursor (Acrogranin) [Contains: Granulin 7]. GRN. Musumalia: Eutheria: Rodentia: Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090; OSCIENCE FROM N.A. MEDLINE-93245991; PubMed-8482392; Baba T., Nemoto H., Watanabe K., Arai Y., Gerton G.L.; Baba T., Nemoto H., Watanabe K., Arai Y., Gerton G.L.; Baba T., Nemoto H., Watanabe K., Arai Y., Gerton G.L.; CAND/Intron organization of the gene encoding the mouse epithelin/granulin precursor (acrogranin)."; Castle Contain Contains C	CC -1- FUNCTION: GRANULINS HAVE POSSIBLE CYTOKINE-LIKE ACTIVITY. THEY WAY CC -1- TISSUB RENCIENTLY. CC -1- TISSUB REPORTERING. CC -1- TISSUB REPORTERING. CC -1- TISSUB REPORTERING. CC -1- TISSUB SPECIFICITY: UBIQUITOUS. CC -1- PTW: GRANULINS ARE DISULFIDE BRIDGED. CC This SWISS-PROT entry is copyright. It is produced through a collaboration complement to the European Bioinformatics and the EMBL outstation on its case by non-profit institutions as long as its content is in no way compactive by non-profit institutions as long as its content is in no way compactive by non-profit institutions as long as its content is in no way compactive by non-profit institutions as long as its content is in no way correct an email to license@isb-sib.ch). CC cor send an email to license@isb-sib.ch/announce/cc cor send an email to license@isb-sib.ch/announce/
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-i- FUNCTION: GRANULINS HAVE POSSIBLE CYTOKINE-LIKE ACTIVITY. THEY MAY PLAY A ROLE IN INFLAMMATION, WOUND REPAIR, AND TISSUE REMODELING.
-i- TISSUE SPECIFICITY: UBIQUITOUS; MOST ABUNDANT IN THE SPLEEN AND SEVERAL TISSUES OF ENDOCRINE SIGNIFICANCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plowman G.D., Green J.M., Neubauer M.G., Buckley S.D., McDonald V.L., Todaro G.J., Shoyab M.;

"The epithelin precursor encodes two proteins with opposing activities on epithelial growth.";
J. Biol. Chem. 267:13073-13078(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Granulin G);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-1992 (Rel. 24, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Granulins precursor (Acrogranin) [Contains: Granulin 1 (Granulin Granulin 2 (Granulin F); Granulin 3 (Granulin B) (Epithelin 2);
Granulin 4 (Granulin A) (Epithelin 1); Granulin 5 (Granulin C);
Granulin 6 (Granulin D); Granulin 7 (Granulin E)].
                                                                                                                          (POTENTIAL)
                                                                                                                                                                    (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 204-225 AND 279-299.
MEDLINE-91045907; Pubmed-2236009;
Shoyab M., McDonald V.L., Byles C., Todaro G.J., Plowman G.D.;
"Epithelins 1 and 2: isolation and characterization of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            distribution, and cellular localization of the rat granulin
                                                                                                                                                                                                                                                    Length 589;
                                                         GRANULIN 6.
GRANULIN 7.

N-LINKED (GLCNAC. ..) (POT

N-REF. 2)

N-REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 204-259 AND 278-334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Systeine-rich growth-modulating proteins.";
Proc. Natl. Acad. Sci. U.S.A. 87:7912-7916(1990)
                                                                                                                                                                                                                                                       Score 89; DB 1;
Pred. No. 6.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            588 AA
                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bhandari V., Giaid A., Bateman A.; "The complementary deoxyribonucleic acid
                                          GRANULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endocrinology 133:2682-2689(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Kidney;
MEDLINE-94062640; PubMed-8243292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Kidney;
MEDLINE-92317004; PubMed-1618805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-91097544; PubMed-2268320;
                                                                                                                                                                                                                                                                                                                                                               1 KKVIAPRRLPDPQILKSDT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20, Created)
24, Last seq
                                                                                                                                                                                                              63458 MW;
                                                                                                                                                                                                                                                                                                 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 278-328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FISSUE-Bone marrow;
                                                                                                                                                                                                            589 AA;
                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1991 (Rel.
01-DEC-1992 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-10116;
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01-DEC-1992
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                                                                                                                          CARBOHYD
CARBOHYD
                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                       Query Match
                                                                                                        CARBOHYD
                                                                                                                                                                      CARBOHYD
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P23785;
                                                              PEPTIDE
                                                                                    PEPTIDE
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                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADBM 8 precursor (EC 3 4-24.-) (A disintegrin and metalloproteinase
domain 8) (Cell surface antigen MS2) (CD156a antigen) (CD156).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yoshiyama K., Higuchi Y., Kataoka M., Matsuura K., Yamamoto S.; CD156 (human ADAM8): expression, primary amino acid sequence, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics 41:56-62(1997).
-1- FUNCTION: POSSIBLE INVOLVEMENT IN EXTRAVASATION OF LEUKOCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: EXPRESSED ON NEUTROPHILS AND MONOCYTES.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113D434F7E099B31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
S -> FP (IN REF. 2.)
TK -> SB (IN REF. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 824 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 0.01; Mismatches
-! - PIM: GRANULINS ARE DISULFIDE BRIDGED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRANULIN 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRANULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRANULIN GRANULIN
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MEDLINE-97271556; PubMed-9126482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343 KKVTASLSLPDPQILKND 360
                                                                                                                                                                                                                                                                                                                                                                                                                                           t; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KKVIAPRRLPDPQILKSD 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata,
Mammalla, Eutheria, Primates,
                                                                                                                                                                                                                                                                                                                                       rik; Esouso; Esouso.
InterPro; IPR000118; Granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63369 MW;
                                                                                                                                                                                                                              EMBL; M97750; AAA16903.1; -. EMBL; X62322; CAA44198.1; -.
                                                                                                                                                                                                                                                                                                                                                                                            100277; GRAN; 7.
PS00799; GRANULINS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.6%;
ilarity 72.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00396; granulin; 7. SMART; SM0277; GRAN; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADAM8 OR MS2.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                           PIR; E36698; E36698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  588 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene location.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AD08_HUMAN
P78325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEPTIDE CARBOHYD CARBOHYD CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADO8_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRN_HUMAN STANDARD; PRT; 593 AA.
P28799; P23781; P23782; P23783; P23784; Q9BWE7;
P28799; Rel. 20, Created)
Ol-NOV-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Granulins precursor (Acrogranin) [Contains: Paragranulin; Granulin 1
(Granulin G); Granulin A); Granulin F); Granulin B);
Granulin 4 (Granulin A); Granulin 5 (Granulin G); Granulin 6 (Granulin
                                                                                                                                         Campos-Garcia J., Caro A.D., Najera R., Miller-Maier R.M., Al-Tahhan R.A., Soberon-Chavez G.;
"The Pseudomonas aeruginosa rhig gene encodes an NADPH-dependent betaketoacyl reductase which is specifically involved in rhamnolipid synthesis.";
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=ATCC 15692 / PAO1;
STRAIN=ATCC 15692 / PAO1;
STRAIN=ATCC 15692 / PAO1;
STRAIN=ATCC 15692 / PAO1;
WEDLINE=2043737; PubMcd=10984043;
Stover C.K., Paha M.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover W.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim.R.M., Bridt K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lorry S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- FUNCTION: REQUIRED FOR THE SINTHESIS OF THE BETA-HYDROXY ACID MOIETY OF RHAMNOLIPIDS.
-i- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
NADP(+) - 3-oxocyl-[acyl-carrier protein] + NADPH.
-i- PATHWAX: Rhamnolipids fatty acid molety biosynthesis.
-i- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
  Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; DB 1; Length 256;
4.7;
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8 MDP (BY SIMILARITY).
0 BY SIMILARITY.
6830 MW; 3DB7B481F34C89A3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

46.4%; Score 44.5;
Best Local Similarity 42.3%; Pred. No. 4.
Matches 11; Conservative 3; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 VIAPGREPSRMTRHIANDPQALEADS 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 VIAPRRLP------DPQILKSDT 19
                                                                                                                                                                                                                                                                          . Bacterioj. 180:4442-4451(1998).
                                                                                      SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-98389657; Pubmed-9721281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002198; ADH_short.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF148964; AAD53514.1; -.
EMBL; AE004760; AAG06775.1; -.
HSSP; P50162; 1AE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26830 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00106; adh_short; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 406:959-964(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               opportunistic pathogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oxidoreductase; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14
160 1
256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SDR) FAMILY.
                                              NCBL_TaxID=287;
                            Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NP_BIND
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRN_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
  g
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                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee(18b-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Rhamnollpids biosynthesis 3-oxoacyl-[acyl-carrier protein] reductase
(EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZINC (CATALYTIC) (PROBABLE).
ZINC (CATALYTIC) (PROBABLE).
SIMILARITY: CONTAINS 1 DISINTEGRIN DOMAIN.
DATABASE: NAME-PROW; NOTE-CD guide CD156 entry;
WWW-"http://www.ncbi.nlm.nlh.gov/prow/cd/cd156.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZINC (CATALYTIC) (PROBABLE)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01186; EGF_2; UNKNÖWN_1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
HYDTOlase; Metalloprotease; Zinc; Signal; Glycoprotein;
Hydromembrane; Antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LINKED (GLCNAC. . .) (PC 5DF8E05F30DF479E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISINTEGRIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METALLOPROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.9%; Score 43.8%; Pred. No. 9.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG PROSITE; PS50214; DISINTEGRIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002870; Pep_M12B_propep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADAM 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001590; Reprolysin.
InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00200; disintegrin; 1.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF01562; Pep_M12B_propep; 1.
Probom; PD000664; Disintegrin; 1.
                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001762; Disintegrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50215; ADAM_MEPRO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000561; EGF-11ke.
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EVVLPRRLPGPRVRRA 45
                                                                                                                                                                                                                                                                          EMBL; D26579; BAA05626.1; -. HSSP; P18619; 1FVL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dest Match
Best Local Similarity 43.00,
Best Local Similarity 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00050; DISIN; 1.
SMART; SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                        MEROPS; M12.208; -. Senew; BGNC:215; ADAM8.
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824 AA;
                                                                                                                                                                                                                                                                                                                                                                       MIM; 602267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RHLG_PSEAE
Q9RPT1;
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TRANSMEM
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CARBOHYD CARBOHYD

RESULT 4
RHLG_PSEAE

ò 셤 DISULFID CARBOHYD

CT_SITE

(ETAL

DOMAIN

DOMAIN

SIGNAL

Gaps

3; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plowman G.D., Green I.M., Neubauer M.G., Buckley S.D., McDonald V.L., Todaro G.J., Shoyab M.;
"The epithelin precursor encodes two proteins with opposing activities on epithelial cell growth.";
J. Biol. Chem. 267:13073-13078(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: IN MYELOGENOUS LEUKEMIC CELL LINES OF PROMONOCYTIC, PROMYELOCYTIC, AND PROBRYTHROID LINEAGE, IN FIBROBLASTS, AND VERY STRONGLY IN EPITHELIAL CELL LINES. PRESENT IN INFLAMMATORY CELLS AND BONE MARROW. HIGHEST LEVELS IN KIDNEY. PTM: GRANULINS ARE DISULFIDE BRIDGED.
                                                                                                                                     TISSUE-bone marrow;
MEDLINE-92179253; PubMed-1542665;
Bhandari V., Palfree R.G.E., Bateman A.;
Misolation and sequence of the granulin precursor cDNA from human bone marrow reveals tandem cysteine-rich granulin domains.";
Proc. Natl. Acad. Sci. U.S.A. 89:1715-1719(1992).
                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_raxID-9606;
                                                                                                                                                                                                                                                                                            Bhandari V., Bateman A.; "Structure and chromosomal location of the human granulin gene."; Blochem. Biophys. Res. Commun. 188:57-63(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Solomon S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Brain;
Yu W., Gibbs R.A.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE.

SEQUELELALOGOTE;

MEDLINE-SI097544; PubMed=2268320;

Bateman A., Belcourt D.R., Bennett H.P., Lazure C., Sol

"Granulins, a novel class of peptide from leukcoytes."

"Granulins, a novel Commun. 173:1161-1168(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 206-233; 281-336; 364-396 AND 442-447.
                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
TISSUE-Cervix, and Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M75161; AAA58617.1; ALT_SEQ.
EMBL; X62320; CAA44196.1; -.
                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Kidney;
MEDLINE=92317004; PubMed=1618805;
                                                                                                                                                                                                                                                             REVISIONS, SEQUENCE FROM N.A. MEDLINE-93038704; PubMed-1417868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF055008; AAC09359.1; -. EMBL; BC000324; AAH00324.1; -. EMBL; BC010577; AAH10577.1; -.
 Granulin 7 (Granulin E)]
                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A38118; GYHU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.
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Jannatipour M., Rokeach L.A.;
"The Schizosaccharomyces pombe homologue of the chaperone calnexin is
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE-95347333; PubMed+7621821;
Parlati F., Dignard D., Bergeron J.J.M., Thomas D.Y.;
"The calnexin homologue cnx1+ in Schizosaccharomyces pombe, is an essential gene which can be complemented by its soluble ER domain.";
EMBO J. 14:3064-3072(1995).
                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                    NOST,; GRANULINS; 7.
8800799; GRANULINS; 7.
Repeat, Glycoprotein; Signal; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                             S -> H (IN REF. 6).
W -> H (IN REF. 6).
4E402BDB16DE2819 CRC64;
                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (PN-LINKED (IN ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
Eukaryota: Fungi: Ascomycota: Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44; DB 1;
Pred. No. 15;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  FTIG-VAR_003445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 29, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     560 AA.
                                                                                                                                             ACROGRANIN.
PARAGRANULIN
                                                                                                                                                                       GRANDLIN 1.
GRANDLIN 2.
GRANDLIN 3.
GRANDLIN 4.
GRANDLIN 6.
GRANDLIN 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                essential for viability.";
J. Biol. Chem. 270:4845-4853(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-972;
MEDLINE-21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-95181485; PubMed-7876257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequ
15-JUN-2002 (Rel. 41, Last anno
                                          InterPro; IPR000118; Granulin.
Pfam; PF00396; granulin; 7.
SMART; SMG0277; GRAN: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KKVIAPRRLPDPQILKSD 18
                                                                                                                                                                                                                                                                                                                                                                                                           63473 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 45.8%;
Best Local Similarity 55.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OR CNX1 OR SPAC3C7.11C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Calnexin homolog precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
            PIR; JC1284; JC1284.
Genew; HGNC:4601; GRN.
MIM; 138945; -.
                                                                                                                                                                                                                                         7496
7573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                              386
593 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                         PROSITE; PS00799;
                                                                                                                   Polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CALX_SCHPO
P36581;
                                                                                                         Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                              ARBOHYD
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                                                                                                                                                                                                                                                                     CARBOHYD
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                                                                                                                                                                                                                                                                                                ARBOHYE
                                                                                                                                                            PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                       /ARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CALX_SCHPO
                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
Q
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Length 560;

Score 43; DB 1;

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RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Squros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McGrean J.,
RA Mconey P., Moule S., Mungall K., Murphy L., Nibbett D., Odell C.,
RA Mconey P., Woule S., Mungall K., Murphy L., Nibbett D., Odell C.,
RA Stelton J., Simmonds M., Squares R., Squares S., Stevens K.,
Relton J., Simmonds M., Squares R., Squares S., Stevens K.,
Relton J., Simmonds M., Squares R., Squares S., Stevens K.,
Raylor R., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
R Eger P., Zimmernann W., Wedler H., Reinhardt R., Pohl T.M.,
R Eger P., Zimmernann W., Wedler H., Rambutt R., Purnelle S.,
R Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
R Dominguez A., Revuelta J.L., Moreno S., Gloux S., Lelaure V., Mottler S.,
R Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
R Shakovski G.V., Ussery D., Barrell B.G., Nurse P.;
R Nature 415:81-800(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYNTHESIZED GLYCOPROTEINS IN THE ENDOPLASMIC RETICULUM. IT MAY ACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IN ASSISTING PROTEIN ASSEMBLY. AND/OR IN THE RETEMTION WITHIN THE
ER OF UNASSEMBLED PROTEIN SUBUNITS. IT SEEMS TO PLAY A MAJOR ROLE
IN THE QUALITY COURTED APPRATUS OF THE ER BY THE RETENTION OF
INCORRECTLY FOLDED PROTEINS.
SUBCELLULAR LOCATION: Type I membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL).
E3B20877333E9123 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: CALCIUM-BINDING PROTEIN THAT INTERACTS WITH NEWLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probom; PD001866; Calreticulin; 1.
PROSITE; PS00804; CALRETICULIN_1; 1.
PROSITE; PS00804; CALRETICULIN_2; 1.
PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
Calctum-binding; Endoplasmic reticulum; Transmembrane; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL) 4 X APPROXIMATE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 X APPROXIMATE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CALNEXIN HOMOLOG.
LUMENAL (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001580; Calreticulin. Pfam; PF00262; calreticulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63466 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00626; CALRETICULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M98799; AAA79757.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U13389; AAA68631.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAB16741.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reticulum.
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TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SIMILARITY: BELONGS TO THE BACTERIAL PHOSPHOLIPASE C FAMILY.
-i- CAUTION: The gene coding for this protein seems to be defective in strain H37Rv where it is interrupted by the insertion of an IS6110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES—M. Luberculosis; STRAIN-H37Rv; MEDLINE-98295997; PubMed-9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeher K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Rown D., Chillingworth T., Connor R., Hornsby T., Jagels K., Kroph A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Statton S., Statton S., Squares R., Statton S., Statton S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Bectphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES-M.tuberculosis; STRAIN-CDC 1551 / Oshkosh; Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Gwonn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ernolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Identification of variable regions in the genomes of tubercle bacilliusing bacterial artificial chromosome arrays."; Mol. Microbiol. 32:643-655(1999).
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBL_TaxID=1773, 1765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Microbiol. 32:643-655(1999).
--- CATALYTIC ACTIVITY: A phosphatidylcholine + H(2)0 = 1,2-
diacylglycerol + choline phosphate.
--- MISCELLANEOUS: POLYMORPHISM WAS DISCOVERED IN THE PHOSPHOLIPASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES-M. bovis; STRAIN-BCG / Pasteur;
MEDLINE-99255698; PubMed-10320585;
Gordon S.V., Brosch R., Billault A., Garnier T., Eiglmeier K.,
                                      ö
                                                                                                                    5
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                             09XB13; 006792;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
Phospholipase C 4 precursor (EC 3.1.4.3).
PLCD OR RV1755C OR MI1799 OR MICX28.21C.
                                                                                                                                                                                                                            514 AA.
                   Pred. No. 20;
3; Mismatches
                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis, and
44.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete genome sequence.";
                                                                                                     5 APRRIPDPQILKSD 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 393:537-544(1998).
                                        7; Conservative
                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium bovis
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                          Matches
                                                                                                                                                                                      RESULT 7
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C -1 SUBCELLUIAN FOOTATION: MITCHEADER.

-1 SUBCELLUIAN: FORTATION: MITCHEADER.

-1 DISABSE: DEFECTS IN PERO AND A COUSE OF SPASTIC PARAPLEGIA-7

(SPG7), A FORM OF AUTOCOMAL RECESSIVE HEREDITARY SPASTIC

(SPG7), A FORM OF AUTOCOMAL RECESSIVE HEREDITARY SPASTIC

(SPG7), A FORM OF AUTOCOMAL RECESSIVE HEREDITARY SPASTIC

(SPINAL CORD DISORDERS CHARACTERIZED BY A SLOW, GRADUAL,

PROCRESSIVE WEAKNESS AND SPASTICITY (STIFFNESS) OF THE LEGS.

INTITAL SYMPTOMS AND INCLIDE DIFFICULTY WITH BALANCE, WEAKNESS AND

STIFFNESS IN THE LEGS, MUSCLE SPASMS, AND DRAGGING THE TOES WHEN

WALKING: IN SOME FORMS OF THE DISORDER, BLADDER SYMPTOMS (SUCH AS

INCOMTINENCE) MAY APPERA, OR THE WEAKNESS AND STIFFNESS MAY SPRRAD

C OTHER PARTS OF THE BODY. RATE OF PROGRESSION AND THE SEVERITY

OF STMPTOMS IS QUITE VARIABLE.

-1 SIMILARITY: BELONGS TO THE RAA FAMILY OF ATPASES.
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European Bioinformatics Institute. There are no restrictions on it
by non-profit institutions as long as its content is in no wa
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MEDIJNE=99408245; PubMed=10480368;
Settasatian C., Whitmore S.A., Crawford J., Bilton R.L.,
Cleton-Jansen A.-M., Sutherland G.R., Callen D.F.;
"Genomic structure and expression analysis of the spastic paraplegia gene, SPG7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-98297350; PubMed-9635427;
Casari G., De Fusco M., Clarmatori S., Zeviani M., Mora M.,
Fernandez P., De Michele G., Filla A., Cocozza S., Marconi R.,
Duerr A., Fontaine B., Ballablo A.;
"Spatic paraplegia and OXPHOS impairment caused by mutations in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     paraplegin, a nuclear-encoded mitochondrial metalloprotease."; Cell 93:973-983(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB 1; Length 514;
Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-UCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Paraplegin (EC 3.4.24.-) (Spastic paraplegia protein 7).
PGN OR SPG7.
                                                                                                                                                                                                                                                                                                                            PHOSPHOLIPASE C 4.
9D99A466D312BA30 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 795 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                           Hydrolase; Signal; Complete proteome
                                                                                           EMBL; Z95890; CAB09340.1; ALT_SEQ.
EMBL; AE007040; AAK46072.1; -;
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                                                                                                                                                                                                                                                                                                                                                           55770 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                            43.8%;
                                                                                                                                                         EMBL; Y18606; CAB44656.1;
TIGR; MT1799; -.
Tuberculist; Rv1755c; -.
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Matches 7; Conservative
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PYRVPDPQIM 498
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Q9UQ90; 075756;
16-0CT-2001 (Rel. 40, C.
16-0CT-2001 (Rel. 40, L.
15-JUN-2002 (Rel. 41, L.
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PGN_HUMAN
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coved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Katinka M., Cossart P., Sibilli L., Saint-Girons I., Chalvignac M.A., 18 Bras G., Cohen G.N., Yaniv M.;
"Nucleotide sequence of the thra gene of Escherichia coll.";
Proc. Natl. Acad. Sci. U.S.A. 77:5730-5733(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKIH_ECOLI STANDARD; PRT; 820 AA.
P00551, Q47659,
21-JUL-1986 (Rel. 01, Last sequence update)
15-CCT-2001 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
18-Includes: Appartokinase I (EC 2.7.2.4); Homoserine dehydrogenase I (Includes: Aspartokinase I (EC 2.7.2.4); Homoserine dehydrogenase I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
BY CINC (CATALYTIC) (BY SIMILARITY).
G -> R (IN REF. 1).
DA63283387517226 CRC64;
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modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@lsb-sib.ch).
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InterPro; IPR000642; Peptidase_M41.
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TIGRFAMS; TIGR01241; FtsH_fam; 1.
                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003593; AAA_ATPase.
                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00004; AAA; 1.
Pfam; PF01434; Peptidase_M41; 1.
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THRA OR THRAI OR THRA2 OR B0002.
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269
356
574
575
578
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88135 M
                                                             EMBL; X16610; CAA76314.1;
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TRANSMEM
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METAL
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EMBL;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENZYME REGULATION: THE ENZYME ACTIVITIES ARE REGULATED ALLOSTERICALLY BY L-THREONINE.
PATHWAY: CATALYZES 2 NONCONSECUTIVE REACTIONS IN THE COMMON BIOSTHTHETIC PATHWAY LEADING FROM ASP TO DIAMINOPIMELATE AND LYS, TO MEY, AND TO THR AND ILE.
SUBGNIT: HOMOTETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS: ASPARTOKINASE II-HOMOSERINE DEHYDROGENASE II AND ASPARTOKINASE III ALSO CATALYZE THE SAME REACTION(S). SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CB
                                                                   Tura T., Mori H., Nagal H., Nagata T., Ishihama A., Fujita N., Isono K., Mizobuchi K., Nakata A.; Systematic sequencing of the Escherichia coli genome: analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zakin M.M., Duchange N., Ferrara P., Cohen G.N.;
J. Biol. Chem. 258:3028-3031(1983).
-!- CATALYTIC ACTIVITY: L-homoserine + NAD(P)(+) = L-aspartate 4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIANE-80043179; PubMed-387092;
Sibilli L., le Bras G., Cossart P., Chalvignac M.A., le Bras G.,
Billey P.A., Cohen G.N.;
"The primary structure of Escherichia coli K 12 aspartokinase I-homoserine dehydrogenase I: sequence of cyanogen bromide peptide
                                                                                                                                                                                                                                                                        "Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes."; Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                                                                MEDLINE-80077291; PubMed-390305;
Cossart P., Katinka M., Yaniv M.;
"Construction and expression of a hybrid plasmid containing the
Escherichia coli thrA and thrB genes.";
Mol. Gen. Genet. 175:39-44(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            semialdehyde + NAD(P)H.
-1- CATALYTIC ACTIVITY: ATP + L-aspartate = ADP + 4-phospho-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASPARTOKINASE FAMILY.
SIMILARITY: IN THE C-TERMINAL SECTION, BELONGS TO THE
HOMOSERINE DEHTDROGENASE FAMILY.
                                                                                                                                                                                SEQUENCE FROM N.A.
STRALN-K12 / MG1655;
MEDLINE-95334562; Pubmed-7610040;
BUTLAND V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                            the 0-2.4 min region.";
Nucleic Acids Res. 20:3305-3308(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; V00361; CAA23660.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVISION TO 11.
MEDLINE-83135751; Pubmed-6298218;
                                                   MEDLINE-92334977; PubMed-1630901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished results, cited by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lochimie 61:733-739(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 51-129.
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                   SEQUENCE FROM N.A.
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V00360; CAA23659.1;

AE000111;

EMBL; EMBL;

014003; D10483;

AAA83914.1; BAA01286.1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acquired immunodeficiency syndrome.";
Virology 157:317-329(1987).
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                              Oxidoreductase; Threonine biosynthesis; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Luciw P.A.;
"Sequence relationships of type D retroviruses which cause simian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
POL polyprotein [Contains: Reverse transcriptase (EC 2.7.7.49);
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MEDLINE-87151131; PubMed-2435057;
Thayer R.M., Power M.D., Bryant M.L., Gardner M.B., Barr P.J.,
                                                                                                                                                                                                                                            enzyme; Multifunctional enzyme; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 820;
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2 -> 0 (IN REF. 3).
4 -> T (IN REF. 3).
5 -> M (IN REF. 3).
6 -> M (IN REF. 3).
7 -> M (IN REF. 3).
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Pred. No. 44;
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                                                                                          IPR001341; Aspartate_kinase.
                                                                                                                                                                                    TICRFAMS; TIGRO0657; asp kinases; 1. PROSITE; PS00324; ASPARTOKINASE; 1. PROSITE; PS01042; HOMOSER_DHGENASE; 1.
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                                                                                                                  nterPro; IPR005106; NAD_binding_3.
fam; PF00696; aakinase; 1.
                                                                                                        IPR001342; Homoserine_dh
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                                                                                                                                                                         NAD_binding_3; 1
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                                               EcoGene; EG10998; thra.
InterPro; IPR002912; ACT.
InterPro; IPR001048; Aa_kinase.
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01-OCT-1996 (Rel. 34, Last sequ
15-JUN-2002 (Rel. 41, Last anno
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58.3%;
          EMBL; M10644; AAA24671.1;
PIR; A00671; DEECK.
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237 PROVPDARLLKS 248
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658
820 AA;
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Les 7; Conserv
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                                      $40531
                                                                                                                                                                                                                                              Allosteric
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P51517;
                                                                                             InterPro;
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Pfam; PF00772; DnaB; 1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endonuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMA-1 OR PF83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMA1_PLAF8
P50492;
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CONFLICT
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     DP
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  entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Definition S.V. Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Elglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock R., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Selston J.E., Skelton S., Squares S., Squares R., "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";

Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Early Haft D., Hickey E.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: THE INTEIN IS AN ENDONUCLEASE (POTENTIAL).
PTM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PARTICIPATES IN INITIATION AND ELONGATION DURING
CHROMOSOME REPLICATION; IT EXHIBITS DNA-DEPENDENT ATPASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Replicative DNA Helicase (EC 3.6.1..) (Contains: Endonuclease PI-MtuHIP (EC 3.1...) (KHU dnaB intein).
MANDA OR WYOOSB OR WICOSA OR WICO
                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF02022; Integrase_Zn; 1.
Transferase; RNA-directed DNA polymerase; Hydrolase; Nuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42; DB 1; Length 867;
Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98038 MW; F64227F7365F3659 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             874 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 47;
3; Mismatches
                               or send an email to license@isb-sib.ch)
                                                                                                                                                                 InterPro; IPR003308; Integrase_Zn
InterPro; IPR002156; RNaseH.
InterPro; IPR000477; RVTse.
InterPro; IPR001584; RVe.
                                                                                                                                    InterPro; IPR001037; Integrase_C.
InterPro; IPR003308; Integrase_Zr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
15-DEC-1998 (Rel. 37, Last sequ
                                                                                 EMBL; M16605; AAA47562.1; -..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 ILAPQRYADPITWKSD 29
                                                                                                                                                                                                                                                                                                                            PF00552; integrase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Endonuclease; Polyprotein.
                                                                                                                                                                                                                                                                         Pfam; PF00075; rnaseH; 1.
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                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00665; rve; 1.
                                                                                                                                                                                                                                                                                                      PF00078; rvt; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              867 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNAB_MYCTU
P71715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                               Pfam;
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
A POST-TRANSLATIONAL EXCISION OF THE INTERVENING REGION (INTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thomas A.W., Waters A.P., Carr D.; "Analysis of variation in PF83, an erythrocytic merozoite vaccine candidate antigen of Plasmodium falciparum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGRAMS; TIGRO0665; DnaB; 1.
PROSITE; PS50818; INTEIN_C_TER; 1.
PROSITE; PS50819; INTEIN_ENDONUCLEASE; 1.
PROSITE: PS50817; INTEIN_N_TER; 1.
DNA replication; DNA-binding; ATP-binding; Hydrolase; Helicase;
Primosome; Protein splicing; Autocatalytic cleavage; Nuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome. REPLICATIVE DNA HELICASE, 1ST PART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENDONUCLEASE PI-MTUHIP.
REPLICATIVE DNA HELICASE, 2ND PART
ATP (POTENTIAL).
A P G (IN REF. 2).
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                      FOLLOWED BY PEPTIDE LIGATION.
SIMILARITY: BELONGS TO THE HELICASE FAMILY: DNAB SUBFAMIL SIMILARITY: IN THE INTEIN SECTION; BELONGS TO THE HOMING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum (isolate 7G8).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=57266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERYTHROCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               894155A86DCB9D70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Blochem. Parasitol. 42:285-287(1990).
-i- FUNCTION: INVOLVED IN PARASITE INVASION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
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16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003587; Hedgehog_hintN.
InterPro; IPR002203; Intein.
InterPro; IPR004042; Intein_endonuc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000229; RecA; 1.
ProDom; PD002663; DnaB_helicase; 1.
SMART; SM00305; Hint; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ruberculist, Rv0058; -.
InterPro, IPR001198; DnaB_helicase.
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MEDLINE=91101665; Pubmed=2270110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE006918; AAK44286.1;
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                                                                                                                            ENDONUCLEASE FAMILY.
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491 RIAAPRRVPEP 501
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REBASE; 4230; PI-MtuHIP.
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EMBL; M27957; AAA29476.1; -. EMBL; A08267; CAA00764.1; -.
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01-0CT-1996
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                                                                                                                               DOMAIN
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AMA1_PLAFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: STRONG TO AMA-1 FROM P.CHABAUDI AND P.FRAGILE, AND TO PR66 FROM P.KNOWLESI.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: STRONG TO AMA-1 FROM P.CHABAUDI AND P.FRAGILE, AND TO
PR66 FROM P.KNOWLESI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Meterson M.G., Marshall V.M., Smythe J.A., Crewther P.E., Lew A., Sliva A., Anders R.K. Kemp D. S.

Integral membrane protein located in the apical complex of Plasmodium falciparum.";

Mol. Cell. Biol. 9:3151-3154(1989).

I. FUNCTION: INVOLVED IN PARASITE INVASION OF ERYTHROCYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Apical membrane antigen 1 precursor (Merozoite surface antigen).
                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 622;
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NCBI_TaxID=5837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                            EMBL; MS8548; AAA29721.1; ...
InterPro; IRO03298; Apmem_Ag1.
Ffam; PF02430; AMA-1; 1.
PRINTS; PR01361; MEROZOTTESA.
Mlaria; Signal; Transmembrane; Antigen; Glycoprotein.
24 POTENTAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum (isolate FC27 / Papua New Guinea)
                                                                                                                                                                                                                                                            APICAL MEMBRANE ANTIGEN 1. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                           1C9C8715D8E2915F CRC64;
                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
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01-AUG-1991 (Rel. 19, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                            71990 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                         43.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           622 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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P22621;
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TRANSMEM
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AMA1_PLAFF
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EMBL; M27133; AAA29475.1; -.

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                                                                                                                                                                                                                                                                          CAL)

COTENTIAL)

(POTENTIAL)

CALCING...) (POTENTIAL)

CALCING...) (POTENTIAL)

(IN REF. 1; AAA29476)

(IN REF. 1; AAA29476)

TO REF. 1; AAA29476)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Apical membrane antigen 1 precursor (Merozoite surface antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum (isolate thtn / Thailand).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=70151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; AAA29476)
F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                               APICAL MEMBRANE ANTIGEN 1.
                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR01361; WEROZOITESA.
Walaria; Signal; Transmembrane; Antigen; Glycoprotein.
                                                                                                       Antigen; Glycoprotein.
                                                                                                                                                                                                                                                                 | N - LINKED (GLCNAC. . . ) (
| N - LINKED (GLCNAC. . . ) (
| N - LINKED (GLCNAC. . . ) (
| N - LINKED (GLCNAC. . . ) (
| N - LINKED (GLCNAC. . . ) (
| N - LINKED (GLCNAC. . . ) (
| N - LINKED (GLCNAC. . . ) (
| O - > E (IN REF. 1; AAA29.
                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                               0 -> E (IN REF. 1; A. I. A. I. A. I. M. REF. 1; A. I. A. I. N. REF. 1; A. H. -> N (IN REF. 1; A. I. A. I. A. I. N. M. REF. 1; A. I. A. I. N. S. I. N. -> K (IN REF. 1; A. I. A. I. A. I. A. I. N. S. I. A. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 39;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KKVIAPR-----RLP-DPQILKSDT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41.5;
                                                                                                                (alaria; Signal; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M58547; AAA29720.1; -.
InterPro; IPR003298; Apmem_Agl.
Pfam; PF02430; AMA-1; 1.
                          InterPro; IPR003298; Apmem_Ag1.
Pfam; PF02430; AMA-1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72009 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.28;
36.78;
                                                                                  PRINTS; PR01361; MEROZOITESA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 36.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
JR; A32499; A32499.
                                                                                                                                                                                                                                                                                                                                                               421
499
3308
332
407
439
496
503
622 AA;
                                                                                                                                                                                                                                                                               162
286
371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i - CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP + dlphosphate + L-glutamyl-tRNA(Glu).
-i - SUBUNIT: MONOMER (BY SIMILARITY).
-i - SUBCELLUTAR LOCATION: Cytoplasmic.
-i - SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M. Wan Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujil C., Cotton M.D., Horst K., Roberts K., Hatch B., Smith H.O., Venter J.C.;
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
                                                                                                                                                                                                                  3; Indels 11;
                                                                                                                                                                                 DB 1; Length 622;
                    EXTRACELLULAR (POTENTIAL)
 APICAL MEMBRANE ANTIGEN 1
                                                                                                                                                 1FDFA53593C94CC5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GluRS).
GLTX OR BB0372.
Borrella burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrella.
                                                               N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                   490 AA.
                                                                                                                                                                               Score 41.5; DE Pred. No. 39; 5; Mismatches
                                                                                                                                                                                                                                                                   1 KKVIAPR-----RLP-DPQILKSDT 19
                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-ATCC 35210 / B31;
MEDLINE-98065943; PubMed-9403685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nterPro; IPR004527; Gltx_bact
                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seq
                                                                                                                                                  71989 MW;
                                                                                                                                                                                 43.28;
                                                                                                                                                                                             Local Similarity 36.7%;
hes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE001142; AAC66742.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aminoacyl-tRNA synthetase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 390:580-586(1997)
                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                  622 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tam; PF00749:
                                                                                                                                                                                                                                                                                                                                                               SYE_BORBU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGRFAMS;
                                TRANSMEM
DOMAIN
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                              CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                051345;
                 DOMAIN
                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                 RESULT 15
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FTTTTTTT
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Length 490;
                                                                                 Indels
        "HIGH" REGION.
"KMSKS" REGION.
ATP (BY SIMILARITY).
E7ED6AD2474934F4 CRC64;
                                                             DB 1;
36;
                                                                       Pred. No. 36;
0; Mismatches
                                                             Score 41;
                                                                                                                                                       completed: July 8, 2003, 16:24:59
ne : 11.2564 secs
         19 "F
255 "R
254 AT
56751 MW;
                                                            42.7%;
88.9%;
                                                           Query Match 42.7
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                ||| ||| |||||
182 PDEVILKSD 190
                                                                                                     10 PDPQILKSD 18
                                         490 AA;
Complete proteome.
SITE 9
                                         SEQUENCE
                    SITE
BINDING
                                                                                                                                                        Search co
  W I I I S
                                                                                                      ö
                                                                                                                          g
```

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd:

OM protein - protein search, using sw model

Run on:

July 8, 2003, 16:17:10 ; Search time 40.9231 Seconds (without alignments) 95.665 Million cell updates/sec

US-09-824-647-3 96 Title: Perfect score:

1 KKVIAPRRLPDPQILKSDT 19 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 seqs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

SPTREMBL_21:* Database :

sp_invertebrate: sp_archea:* sp_bacteria: sp_mammal:* sp_human:* sp fund1:

sp_unclassified: sp_rvirus:* sp_bacteriap:* sp_vertebrate: sp_organelle: sp_plant:* sp_rodent: p_virus:* sp_phage:* sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

	-		Description	Q9d2v3 mus musculu	O86149 campylobact	Q9png3 campylobact	Q9k5d5 campylobact	Q9n4k2 caenorhabdi	. Q8qvc6 colorado ti	Q9enk9 colorado ti	Q9h8s1 homo sapien	Q13648 homo sapien	Q9hbt9 homo sapien	Q8tnc8 methanosarc	064621 arabidopsis	Q99p28 mus musculu	Q40159 lycopersico	080056 staphylococ	Q9f0g6 pseudomonas
SUMMARIES			ΩI	Q9D2V3	086149	Q9PNG3	Q9K5D5	Q9N4K2	Q8QVC6	Q9ENK9	Q9H8S1	013648	.09нвт9	Q8TNC8	064621	Q99P28	040159	080056	Q9F0G6
			DB	11	~	16	7	ນ	12	12	4	4	4	17	10	11	10	σ	7
			Match Length DB	589	328	328	330	755	482	684	413	463	466	1300	131	164	174	223	255
	œ	Query	Match	92.7	50.0	50.0	50.0	46.9	46.4	46.4	45.8	45.8	45.8	45.8	44.8	44.8	44.8	44.8	44.8
			Score	68	48	48	48	45	44.5	44.5	44	44	44	44	43	43	43	43	43
		Result	No.	1	7	m	₹	'n	9	7	œ	6	10	11	12	13	14	15	16

annotation of a full-length mouse cDNA collection.";

EMBL; AK018744; BAB31384.1; -.

	4		Q9vwd0 drosophila	Q8squ0 encephalito			Q95rng drosophila				Q9fw59 oryza sativ		Q53641 sulfolobus	8	O62677 saimiri sci	O62678 actus trivi	Q9n8i4 trypanosoma	Q9v4n9 drosophila	Q9n8i2 trypanosoma	(1)	Q8zs19 salmonella	Q8z9r7 salmonella	Q8xa84 escherichia	Q9wq04 simian retr	Q9wq00 simian retr	. Q26816 trypanosoma	Q8wpt4 trypanosoma	. Q8wpt3 trypanosoma
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Q9D1F2	09A244	Q9H1R3	00MA60	OBSONO	Q8SDK4	Q8T2E3	095RN4	P73818	Q9W045	097CD6	Q9FW59	Q9YUR2	053641	P71838	062677	062678	Q9N814	09V4N9	Q9N812	Q8RMX0	982819	Q829R7	Q8XA84	Q9WQ04	09WQ00	026816	Q8WPT4	Q8WPT3
11	16	4	'n	ห	6	ស	ហ	16	ស	11	10	12	-	16	ø	9	Ŋ	'n	'n	~	16	19	16	15	15	S	Ŋ	2
271	344	296	692	851	1550	1789	124	244	298	305	465	202	556	999	627	632	644	644	780	820	820	820	/820	867	867	1650	1657	1657
44.8	44.8	44.8	44.8	44.8	44.8	44.8	43.8	43.8	43.8	43.8	43.8	43.8	43.8	43.8	43.8	43.8	43.8	43.8	43.8	43.8	43.8	43.8	43.8	43.8	43.8	43.8	43.8	43.8
43	43	43	43	43	43	43.	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arawawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H., Sissi C., King B., Kochiwa H.,
Richi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schrimi L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,
Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Brons P., Marchlonni L., Mashima J., Mazzarelli J., Momberts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Whynshaw-Boolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
M. Winshaw-Boolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus NCBL_TaxID=10090; 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Adult male kidney CDNA, RIKEN full-length enriched library, 589 AA. 17, Created) PRT; STRAIN-C57BL/6J; TISSUE-KIDNEY; MEDLINE-21085660; PubMed-11217851; PRELIMINARY; 01-JUN-2001 (TrEMBLrel. 01-JUN-2001 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel. musculus (Mouse) [1] SEQUENCE FROM N.A. **09**D2V3 RESULT 1

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RESULT 2 086149 ID 0861

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Length 328;

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Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C., Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Gouail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M., Whitehead S., Barrell B.G., Whitehead S., Barrell B.G., The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fry B.N., Korolik V., van der Zeijst B.A., Coloe P.J.; *A gene cluster from Campylobacter jejuni involved in inner core and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
NCBL_TaxID-197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AJ131360; CAC01389.1; -. HSSP; P09147; 1XEL.
Interpro; IPRO1509; Epimerase_Dh.
Pfam; PF01370; Epimerase; 1.
TIGRFAMS; TIGR01179; galE; 1.
SEQUENCE 330 AA; 37053 MW; 143E592891246F9E CRC64;
                                                                                                                                                                                                                                                                                                    328 AA; 36734 MW; 7372DDC08F8F5676 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TTEMBLrel. 15, Last sequence update) 01-JUN-2002 (TTEMBLrel. 21, Last annotation update) Hypothetical 81.7 kDa protein.
                                                                                                                                                                                                                                                                                                                                   Score 48; DB 16;
Pred. No. 7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 50.0%; Score 48; DB 2; Best Local Similarity 55.6%; Pred. No. 7.5; Matches 10; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              330 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   755 AA.
                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                               reveals hypervariable sequences.";
Nature 403:65-668(2000).
EMBL; AL139077; CAB73386.1; -.
HSSP: P09147; IKVS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                            InterPro; IRRO01509; Epimerase_Dh.
Pfam; PF01370; Epimerase; 1.
TIGREAMS; TIGRO1179; galE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297
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                                                                                                                                                                                                                                                                                                                                                                                                                               1 KKVIAPRRLPDPQILKSD 18
                                                                                                                                                                                                                                                                                                                                           55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 :||{| || || || || || || || || || 280 KVELAPRRAGDPSVLISD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 55.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UDP-glucose 4-epimease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A synthesis.";
                                                                                                                                                                                                                                                                                  Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-81116;
                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                              Query Match
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Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fry B.N., Korolik V., ten Brinke J.A., Pennings M.T.T., Zalm R., Teunis B.J.J., Coloe P.J., van der Zeijst B.A.M.;
"The lipopolysaccharide biosynthesis locus of Campylobacter jejuni
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                                                                                                                                                                                          Query Match 92.7%; Score 89; DB 11; Length 589; Best Local Similarity 94.7%; Pred. No. 2.2e-06; Matches 18; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB 2; Length 328;
Pred. No. 7.5;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001509; Epimerase_Dh.
Pfan; PF01370; Epimerase; 1.
TIGRPAMS; TIGR01179; galE; 1.
SEQUENCE 328 AA; 36791 MW; FA49B77EC02793AA CRC64;
                                                             Pfan; PF00396; granulin; 7.
SWART; SW00277; GRAN; 7.
PROSITE; PS00199; GRANULINS; 7.
SROGTE; PS00118; PAZ_HIS; UNKNOWN_1.
SEQUENCE 589 AA; 63405 MW; 1DE8229C413CA292 CRC64;
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Last annotation update)
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                 InterPro; IPR000118; Granulin.
InterPro; IPR001211; PhospholipaseA2
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STRAIN-NCTC 11168;
MEDLINE-20150912; PubMed-10688204;
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                                                                                                                                                                                                                                                                                                      344 KKVIAPLRLPDPQILKSDT 362
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EMBL; Y11648; CAA72350.1; -.
HSSP; P09147; 1XEL.
                                                                                                                                                                                                                                                                              1 KKVIAPRRLPDPQILKSDT 19
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280 KVELAPRRAGDPSVLISD 297
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21,
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Matches 10; Conservative
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NCBI_TaxID=197;
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086149;
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SO DR REFERENCE OF SOR DR

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RESULT Q9PNG3

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Length 330;

684 AA.

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MEDLINE=20351236; PubMed=10891382; Attoul H., filloir F., Biagini P., Cantaloube J.F., de Chesse R., Attoul H., filloir F., Biagini P., Cantaloube J.F., de Chesse R., De Micco P., de Lamballerie X.; Squence Determination and Analysis of the Full-Length Genome of Colorado Tick Fever Virus, the Type Species of Genus Colivius (Family Reoviridae)."; Biochem. Blophys. Res. Commun. 273:1121-1125(2000).

EMBL; AR139763; AAG00072.1; --
SEQUENCE 684 AA; 76236 MW; 8FE2516BB344B4C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44.5; DB 12; Length 684;
Pred. No. 61;
4; Mismatches 3; Indels 1.
                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                    dsRNA viruses; Reoviridae; Coltivirus
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511 VAPSQAPDPEELLDSDT 527
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les 9; Conserved
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nilarity 55.6%;
Conservative
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                                                  01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                             Colorado tick fever virus
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PRELIMINARY;
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nes 10; Conserv
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Q9H8S1;
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MEDININE-21954629; PubMed=11958454;
Attoul H., Mohd J.F., Biagini P., Cantaloube J.F., de M.P.,
Murphy F.A., de L.X.;
"Genus Coltivirus (family Recviridae): genomic and morphologic
characterization of Old World and New World viruses.";
Arch. Virol. 147:53-561(2002).
EMBL: AF343057; AAM18363:1;
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                                                                                                                                                             "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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Pred. No. 56;
3; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                         Goela D., Miller N., Latreille P., Scheet P.; "The sequence of C. elegans cosmid F54A3."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Direct Submission.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
EMBL; ACO24136; AAF35961.1; --
HSSP: P35520; 1UBQ.
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482 Aa; 53907 MW; 354BA204FADA279F CRC64;
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Last annotation update)
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Colorado tick fever virus.
Viruses; dsRNA viruses; Reoviridae; Coltivirus.
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Best Local Similarity 52.9%; Pred. No. 43;
Matches 9; Conservative 4; Mismatches
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Pfam; PF00291; PALP; 2.
Hypothetical protein.
SEQUENCE 755 AA; 81678 NW; 04290
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                                                                                    STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
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388 VAPSQAPDPEELLDSDT 404
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  NCBI_TaxID-6239;
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01-JUN-2002
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SEQUENCE
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TISSUE-OVARIAN CARCINOMA;
TISSOGA T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sato H., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Raku Y., Rodaira H., Rondo H., Sugawara M.
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Tamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninnolya K., Iwayanagi T.;
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                                                                                                                              Homo sapiens (Human).
Eukaryota: Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 44;
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK023348; BAB14535.1;
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InterPro; IPR001211; PhosphollpaseA2.
Pfam; PF00396; granulin; 4.
SMART; SM00277; GRAN; 4.
PROSITE; PS00799; GRANULINS; UNKNOWN_4.
PROSITE; PS00118; PA2_HIS; UNKNOWN_1.
SEQUENCE 413 AA; 44132 MW; 0B3767A44BB314EC CRC64;
                              Last sequence update)
Last annotation update)
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Matches 8; Conservative
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STRAIN-CV. COLUMBIA;
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Blechschmidt K., Schudy A., Kalaydjieva L., Gooding R., Gresham D.,
Baas F., Jonge, Rd, Schilhabel M.B., Menzel U., Baumgart C.,
Bette M.D., Jahn N., Rosenthal A.;
"Chromosome 8 genomic sequence.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                    O'Hern P.A., Yavetz H., Moy T., Yavetz B., Liang Z.G., Wang G.Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Sequencing Center Jena;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF216667; AAG33017.1; -.
                                                                                                                                                                                                                                                               Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases. EMBL; U60666; AAB02976.1; -... InterPro; IPR001611; LRR.
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                                                                          01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Testis specific leucine rich repeat protein.
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 4;
Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                               Created)
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                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                            SMART; SM00370; IRR; 2.
SMART; SM00446; IRRCap; 1.
SEQUENCE 463 AA; 53936 MW;
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InterPro; IPR003592; LRR_out.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001611; LRR.
InterPro; IPR003603; LRRcap.
InterPro; IPR003592; LRR_out.
Pfam; PF00560; LRR; 3.
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                                  PRELIMINARY;
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                                                                                                                                            Homo sapiens (Human).
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Matches 8; Conserv
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Best Local Similarity
Matches 8; Conserv
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01-JUN-2002
                                                             01-NOV-1996
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                              013648
                                                                                                                           TSLRP.
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Q9HBT9
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RESULT 9
Q13648
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Fitzhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A., Fitzhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A., Allen N., Naylor J., Stange-Thomann N., DeArellanc K., Johnson R., Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W., Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M., Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C., Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I., Metcalf W.W., Birren B.; The, genome of Methanosarcina acetivorans reveals extensive metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D.,
Somerville C.R., Venter J.C.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 1300 AA; 148273 MW; 591A14D4B8AA7EA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
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Last annotation update)
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50.0%; Pred. No. 1.5e+02;
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                                                                                                                                                                                                      1300 AA
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MEDLINE-21929760; PubMed-11932238;
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01-JUN-2002 (TEMBLrel. 21, Last seq
01-JUN-2002 (TEMBLrel. 21, Last ann
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434 EKKHTPRRRPEPKIIPSE 451
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Genome Res. 12:532-542(2002).
EMBL; AE010925; AAM05750.1;
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                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
Hypothetical protein MA2362.
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us-09-824-647-3.rspt

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MEDLINE-9832719; PubMed=9666077;
Raneko J., Kimura T., Narita S., Tomita T., Ramio Y.;
Raneko J., Kimura T., Narita S., Tomita T., Ramio Y.;
Raneko J., Kimura T., Narita S., Tomita T., Ramio Y.;
Raneko J., Kimura T., Narita S., Tomita T., Ramio Y.;
Raneko J., Kimura T., Narita S., Tomita T., Ramio Y.;
Raneko J., Raneko J., Pateriophage phi PVL carrying Panton-Valentine laukocidin genes.*;
Rane 215:57-67(1998).
EMBL; AB009866; BAA31890.1; --
SEQUENCE 223 AA; 25197 MW; 3E91EE45EA9CS638 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          "A molecular study of Meloidogyne incognita-induced feeding sites.";
Plant J. 9:45-54(1996).
                                                                                                                                                       Lycopersicon esculentum (Tomato).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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                                                                                                                                                                                                                                                                                         STRAIN-MARMANDE; TISSUE-MELOIDOGYNE INCOGNITA-INDUCED ROOT KNOT; MEDLINE-96158345; PubMed-8580972; Van der Eycken W., De Almeida Engler J., Inze D., Van Montagu M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
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Van der Bycken W.V.;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                 01, Last sequence update)
21, Last annotation update)
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Pred. No. 26;
5; Mismatches 4
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Conservative 1; Mismatches
                                       174 AA
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                                                                                                                                      Late embryogenesis (Lea)-like protein.
                                                                              (TrEMBLrel. 01, Created)
                                       PRT;
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Best Local Similarity 47.1%;
Matches 8; Conservative
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InterPro; IPRO04864; LEA_2.
Pfam; PF03168; LEA_2; 1.
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                                       PRELIMINARY;
                                                                            01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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Matches 8; Conserv
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01-NOV-1998
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RESULT 14
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SOUTHWICK A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
                                                                                                                                                                           Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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*Multiple Signaling Interactions of Abl and Arg Kinases with EphB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor "; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
  Lin X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                     Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 131 Aa; 14339 MW; 3A33878DC8169802 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Pred. No. 19;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11arity 57.1%; Pred. No. ... Conservative 2; Mismatratri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AC003673; AAC09038.2; EMBL; AY059891; AAL24373.1; EMBL; AX093348; AAM13347.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KKVIAPRRLPDPQILKS 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF339052; AAK08120.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 PRRLPDPQILKSDT 19
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PLRAPDPAITESDS 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarion hes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   musculus (Mouse).
                                                            SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARG (Fragment).
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099P2B

RESULT 13

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Search completed: July 8, 2003, 16:27:56 Job time: 43.9231 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 8, 2003, 16:08:55; Search time 30 Seconds (without alignments) 53:300 Million cell updates/sec Run on:

US-09-824-647-4 69 1 PDAKTQCPDDST 12 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

908470 seqs, 133250620 residues Searched:

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/SIDS2/gcgdata/geneseg/genesegp-embl/AA2000.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA2001.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA2002.DAT:* /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1998.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT: /SIDS2/gcgdata/geneseq/genesegp-embl/AA1985.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981. /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988. /gcgdata/geneseq/geneseqp-embl/AA1990 emb1/AA1994 /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997 gcgdata/geneseq/geneseqp-emb1/AA199 /gcgdata/geneseg/genesegp-embl/AA199 /gcgdata/geneseq/geneseqp-embl/AA199 /qcqdata/geneseq/geneseqp gcgdata/geneseg/genesegp 'gcgdata/geneseq/geneseqp /SIDS2/gcgdata/geneseg A_Geneseq_101002:* /SIDS2 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

hesprintion	oradinesa a	Mouse GP88	Rat epithe	Mouse epith	Mouse GP88	Mouse granu	Granulin B.	Human epithelin pr	Granulin se	Human GP88	Human granu
	,	AAW85477	AAR14325	AAR14327	AAW85474	AAE20520	AAR41880	AAR14326	AAR48673	AAW85475	AAE20521
· E	3 !	20	12	13	50	23	14	12	14	20	23
% Query Watch Longth DB (ID)	The state of the s	12	589	589	589	589	26	593	593	593	593
Query	11000	100.0	100.0	100.0	100.0	100.0	73.9	73.9	73.9	73.9	73.9
. 1000	2000	69	69	69	69	69	51	51	51	51	51
Result		-1	7	٣	4	S	9		8	6	10

ncer		Rat CNK1 protein k	Propionibacterium	Propionibacterium	Peptide #7330 enco	Human brain expres	Human bone marrow	Peptide #7453 enco	Human peptide enco		Human albumin fusi	Vesicular stomatit	_	ъ	Canine IgA. Canis	Listeria monocytog	Novel human diagno	Vesicular stomatit	Eucalyptus grandis	Bovine epithelin p	Amino acid sequenc	4625	Peptide #4725 enco	Protein #4519 enco	Human brain expres	H	#4624	Peptide #4724 enco		ש		u		Arabidopsis thalia	
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AAB43971	AAR41886	AAW01792	AAU61612	AAU42060	ABB39824	AAM60551	AAM73207	AAM33416	ABG43054	AAB87388	ABG65366	AAB20288	ABP28856	ABG15111	AAR97754	ABB49837	ABG03476	AAB20290	AAB16327	AAR15426	AAY93769	ABB31974	ABB37219	ABB22520	AAM57928	AAM70351	AAM18190	AAM30687	AAM05811	ABG39996	AAG31665	AAB20289	AAG31664	AAG31663	
21	14	18	22	22	22	22	22	22	23	22	23	22	23	22	17	23	22	22	21	12	21	22	22	22	22	22	22	22	22	23	21	22	21	21	
621	57	265	121	323	37	37	. 37	37	37	94	94	234	258	322	339	351	446	511	118	179	318	398	398	398	398	398	398	398	398	398	474	511	541	583	
73.9	62.3	59.4	58.0	56.5	55.1	55.1	55.1	55.1	55.1	. 55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	53.6	53.6	53, 6	53.6	53.6	53.6	53.6	53.6	53.6	53.6	53.6	53.6	53.6	53.6	53.6	53.6	
51	43.	41	40	39	38	38	38	38	38	38	38	38	38	38	38	38	38	38	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	
11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

AAW85477 standard; Peptide; 12 AA. AAW85477; RESULT 1

15-MAR-1999 (first entry)

Mouse GP88 autocrine growth factor antigenic peptide P12T.

GP88; granulin; epithilin; mouse; growth factor; autocrine; tumour; cancer; viral infection; antagonist; therapy; diagnosis; antigen; antibody.

Mus sp.

WO9852607-A1.

26-NOV-1998.

98WO-US10555. 22-MAY-1998; 970S-0991862. 970S-0863079. 16-DEC-1997; 23-MAY-1997;

(SERR/) SERRERO G.

Serrero G;

WPI; 1999-045276/04.

Composition containing antagonist of growth factor GP88 - useful for treating cancer and viral diseases and also for diagnosing disease

us-09-824-647-4.rag

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ET-1 is a bifunctional growth regulator, capable of stimulating the growth of some cell types while inhibiting the growth of others. ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory bioactivity. In contrast, however, ET-2 is apparently not capable of eliciting the growth stimulatory activity characteristic of ET-1 and, in fact, antagonises, this ET-1 activity.

See also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20.
                                                                                                                                                                                                                                                          New cysteine rich growth modulating proteins, epithelins - useful as inhibitors of neoplastic cell growth and to promote wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 69; DB 12;
ilarity 100.0%; Pred. No. 0.0048;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           growth regulation; inhibition; stimulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "claim 23, page 55"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP 'claim 25, page 55"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= EP
/note= "claim 27, page 56"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= EP-1
/note= "claim 22, page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "claim 24, page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 18; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362.416
/label-EP
/note-"claim 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= precursor
/note= "claim 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR14327 standard; Protein; 589
91WO-US02321.
                                          910S-0083796.
                                                                                                                                                                                                                                                                                                       healing and treat psoriasis
                                                                                                       BRIM ) BRISTOL-MYERS SQUIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label- EP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse epithelin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 PDAKTQCPDDST 12
|||||||||||||||
208 PDAKTQCPDDST 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label-
                                                                                                                                                    Shoyab M, Plowman GD;
                                                                                                                                                                                             WPI; 1991-325168/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                   N-PSDB; AAQ14338
03-APR-1991;
                                          13-MAR-1991;
03-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR14327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                         GP88 is an 88
                                                                            This is the amino acid sequence of peptide P12T, comprising amino acid residues P208-T219 of murine GB88 (see AAM85474). GP88 is an 88 kba glycoprotein autocrine growth factor that is expressed in a tightly requiated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which acts as a stringently required growth stimulator for the rumorigenic cells. P12T was used in an attempt to raise neutralising antibodies to GP88 (see also AAW85478-79). Antagonists to GP88, such as anti-GP88 antibodies, are used to treat diseases associated with increased expression of GP88, particularly cancer but also viral infections. Anti-GP88 antibodies can also be used and diagnostic reagents and to deliver toxins or other compounds to
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 69; DB 20;
100.0%; Pred. No. 7.9e-05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ET; growth regulation; inhibition; stimulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= EP-1
/note= "claim 12, page 54"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102.416
| Tabel = EP
| Thote= "claim 16, page 54"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "claim 14, page 54"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nabel EP
note- "claim 15, page 54"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note- "claim 13, page 54"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label- precursor
/note- "claim 11, page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR14325 standard; Protein; 589 AA.
                                      Example 8; Page 45; 86pp; English.
from altered GP88 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label- EP-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat epithelin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Watches 12; Conservat
                                                                                                                                                                                                                                                                                                                                               GP88-expressing cells
                                                                                                                                                                                                                                                                                                                                                                                      12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus rattus.
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                                                                                                                                                                                                                                                                                                                                                                                          Seguence
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RESULT 2
AAR14325
ID AAR1

g

Protein

Protein

Protein

Peptide

Pept1de

Peptide

Peptide

Peptide

Gaps

ö

Length 589; Indels 煮.

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This is the amino acid sequence of murine GP88, an 88 kDa glycoprotein autocrine growth factor and epithilin/granulin precursor that is expressed in a tightly regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which acts as a stringently required growth stimulator for the tumorigenic cells. Inhibition of GP88 compared in the tumorigenic cells results in an inhibition of the tumorigenic properties of the overproducing cells. Murine GP88 cDNA (see AAV82824) was obtained from the highly tumorigenic PC cell line. Antagonists to GP88 are used to treat classes associated with increased expression of GP88, particularly cancer but also viral infections. Fragments of GP88 are used to rease specific antibodies (used as antagonists, as diagnostic raspents and for delivering toxins or other compounds to GP88. Cexpressing cells) and to screen for antibodies. Methods are provided for diagnosing disease, or determining susceptibility to disease, resulting from altered GP88 activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse; granulin precursor; GP88; cytostatic; tumourigenicity; tamoxifen; antineoplastic; antioestrogen therapy; skin cancer.
                                                                                                                                                                                                                                                                                                                          Composition containing antagonist of growth factor GP88 - useful for treating cancer and viral diseases and also for diagnosing disease from altered GP88 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Unknown
/note= "Encoded by ATG"
344. 362
/note= "Regions used as antigens to raise anti-GP88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse granulin/epithelin precursor (GP88) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 69; DB 20;
100.0%; Pred. No. 0.0048;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          Example 5; Fig 8A-D; 86pp; English.
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                                                                                                98WO-US10555
                                                                                                                                  970S-0991862.
970S-0863079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 PDAKTQCPDDST 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 PDAKTQCPDDST 12
                                                                                                                                                                                                                                                                      WPI; 1999-045276/04.
N-PSDB; AAV82824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 589 AA;
                                                                                                                                                                                              (STERRY) SERRERO G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                    WO9852607-A1
                                                                                                                                  16-DEC-1997;
23-MAY-1997;
                                                                                                22-MAY-1998;
                                                          26-NOV-1998
                                                                                                                                                                                                                                    Serrero G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE20520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE20520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ET-1 is a bifunctional growth regulator, capable of stimulating the growth of some cell types while inhibiting the growth of others. ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory bloactivity. In contrast, however, ET-2 is apparently not capable of eliciting the growth stimulatory activity characteristic of ET-1 and, in fact, antagonises this ET-1 activity. See also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GP88; granulin; epithilin; mouse; growth factor; autocrine; tumour; cancer; viral infection; antagonist; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                        New cysteine-rich growth modulating proteins, epithelins - useful as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "K19T peptide, used to raise antibody"
562..575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 69; DB 12; Length 589; 100.0%; Pred. No. 0.0048; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "S14R peptide, used to raise antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "P12T peptide used to raise antibody"
144..362
515..570
/label= EP
/note= "claim 28, page 56"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "encoded by CTG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "encoded by AGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note- encoded by TGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW85474 standard; Protein; 589 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse GP88 autocrine growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 23; 97pp; English.
                                                                                                                                                                                              91US-0083796.
                                                                                                                                                                                                                                                    BRIM ) BRISTOL-MYERS SQUIB
                                                                                                                                                        91WO-US02321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1111111111
208 PDAKTQCPDDST 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 PDAKTQCPDDST 12
                                                                                                                                                                                                                                                                                              Plowman GD;
                                                                                                                                                                                                                                                                                                                                WPI; 1991-325168/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
hes 12; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                589 AA;
                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAQ14340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                              13-MAR-1991;
03-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAR-1999
                                                                                                                                                        03-APR-1991;
                                                                              WO9115510-A
                                                                                                                  17-0CT-1991
                                                                                                                                                                                                                                                                                              Shoyab M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW85474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
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      Peptide
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
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Gaps

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Length 589; Indels

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The granulin inhibits keratinocytes and is useful in formulations for promoting the healing of wounds. This peptide was designated granulin B.
                                                                                                                                                                                                                                                                         New cystine rich granulin peptide(s) from leucocyte(s) - are keratinocyte inhibitors useful topically for wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 14; Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ET; growth regulation; inhibition; stimulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 51; DB 14
Pred. No. 0.34;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4, page 53*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282..337
/label= EP-1
/note= "claim 2, page 53"
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/note= "claim 7, page 53"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= EP-2
/note= "claim 3, page 53"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR14326 standard; Protein; 593 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "claim 6,
                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 28; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= EP
/note= "claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= EP
/note= "claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.9%;
                                                  92WO-CA00089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- EP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JAN-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hyman epithelin precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24..180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 PDAKTOCPDDST 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||||:::||| ||
|4 PDARSRCPDGST 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Local 8; Conserve
                                                                                                                                                                                                                           WPI; 1993-320328/40.
                                                                                                                                 (solo/) solomon s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 AA;
                                                  28-FEB-1992;
                                                                                            03-FEB-1992;
         05-AUG-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9115510-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human. The method comprises obtaining a biological sample containing cells from the patient, detecting GPB8 in the cells of the sample, and determining the number of GPB8 positive cells in the sample, and determining the number of GPB8 positive cells in the sample, and determining the ratio of GPB8 positive cells to the total number of cells in the sample. The invention also relates to a method for determining in the sample. The invention also relates to a method for determining anticostrogen therapy. The method is useful for diagnosing tumourigenicity in a sample, such as blood, serum, plasma, urine, nipple aspirate, cerebrospinal fluid, liver, kidney, breast, bone, brain, lung, colon, or skin cancer. The method can be used to treat or prevent re-occurrence of cancer in a patient, by administering tamoxifen if the sample contains less than 10 % GPB8, or less than 5 % GPB8 positive cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diagnosing tumorigenicity in a human, comprising obtaining a cell sample, detecting GP88 in the cells, and determining the number of GP88 positive cells in the sample -
antibodies"
562..575
/note= "Regions used as antigens to raise anti-GP88
antibodies"
586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Granulin; keratinocytes; wound healing; inhibition; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 69; DB 23; Best Local Similarity 100.0%; Pred. No. 0.0048; Matches 12; Conservative 0; Mismatches 0;
                                                                                                                 ACA.
                                                                                                              /note= "Encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      · AAR41880 standard; peptide; 56 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 8; 50pp; English
                                                                                                                                                                                                                                                15-JUN-2001; 2001US-0880842,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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208 PDAKTQCPDDST 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 PDAKTQCPDDST 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          granulocytes; leucocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-267529/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            589 AA;
                                                                                                                                                                                                                                                                                                                                                               (SERR/) SERRERO G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAD32849
                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                            23-MAY-1997;
08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-APR-1994
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Composition containing antagonist of growth factor GP88 - useful for treating cancer and viral diseases and also for diagnosing disease from altered GP88 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is the amino acid sequence of human GP88, an 88 kDa glycoprotein autocrine growth factor and epithilin/granulin precursor that is expressed in a tightly regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which acts as a stringenity required growth stimulator for the tumorigenic cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GP88; granulin; epithilin; human; growth factor; autocrine; tumour; cancer; viral infection; antagonist; therapy; diagnosis.
                                                                                                                               The granulin inhibits keratinocytes and is useful in formulations for promoting the healing of wounds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression or action in the tumorigenic cells results in an inhibition of the tumorigenic properties of the overproducing
                                               New cystine rich granulin peptide(s) from leucocyte(s) - are keratinocyte inhibitors useful topically for wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "A14R peptide used to raise antibody"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
340...364
//note= "E19V peptide used to raise antibody"
566..579
                                                                                                                                                                                                              Length 593;
                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                DB 14;
                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                         Score 51;
Pred. No. 4
                                                                                                  Disclosure; Figure 4c; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                AAW85475 standard; Protein; 593 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human GP88 autocrine growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 5; Fig 9A; 86pp; English.
                                                                                                                                                                                                                73.98;
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97US-0863079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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|PDARSRCPDGST 220
                                                                                                                                                                                                                                                                                1 PDAKTQCPDDST 12
                                                                                                                                                                                                                                                Conservative
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WPI; 1993-320328/40.
N-PSDB; AAQ49052.
                                                                                                                                                                                                                               Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SERR/) SERRERO G.
                                                                                                                                                                              593 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAV82825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9852607-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-NOV-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                AAW85475;
                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                               209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eptide
                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                 AAW85475
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                                                                                                                                                                                                                                                                                                                                             ET-1 is a bifunctional growth regulator, capable of stimulating the growth of some cell types while inhibiting the growth of others. ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory bioactivity. In contrast, however, ET-2 is apparently not capable of eliciting the growth stimulatows extivity characteristic of ET-1 and, in fact, antagonises this ET-1 activity. See also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                New cysteine-rich growth modulating proteins, epithelins - useful as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Granulin; keratinocytes; wound healing; inhibition; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Glycine encoded by CAG."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Valine encoded by ATG."
539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 51; DB 12;
Pred. No. 4.1;
3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR48673 standard; Protein; 593 AA.
                                                                                                                                                                                                                                                                                                               Disclosure; Fig 22; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.9%;
66.7%;
                                                                                                                                  (BRIM ) BRISTOL-MYERS SQUIB.
                                                    91WO-US02321
                                                                                  91US-0083796
90US-0504508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-APR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111:::111 11
209 PDARSRCPDGST 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 66.7
hes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 PDAKTOCPDDST 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              granulocytes; leucocytes
                                                                                                                                                                Shoyab M, Plowman GD;
                                                                                                                                                                                                 WPI; 1991-325168/44.
N-PSDB; AAQ14339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 593 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Granulin sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SOLO/) SOLOMON S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                    03-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-FEB-1992;
                                                                                 13-MAR-1991;
03-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09315195-A
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                    17-0CT-1991
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AAR48673;

RESULT 8 AAR48673

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Sequence Query Match

Best Loc Matches

Solomon S;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       precursor; GP88; cytostatic; tumourigenicity; tamoxifen; antioestrogen therapy; skin cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosing tumorigenicity in a human, comprising obtaining a cell sample, detecting GP88 in the cells, and determining the number of GP88 positive cells in the sample –
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Region used as antigen to develop anti-human GP88 neutralising antibody"
                                                                                      antibodies (used as antaqonists, as diagnostic reagents and for delivering toxins or other compounds to GP88-expressing cells) and to screen for antibodies. Methods are provided for diagnosing disease, or determining susceptibility to disease, resulting from
cells. Antagonists to GPB8 are used to treat diseases associate with increased expression of GPB8, particularly cancer but also viral infections. Fragments of GPB8 are used to raise specific
                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                             20; Length 593;
                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human granulin/epithelin precursor (GP88) protein.
                                                                                                                                                                                                                                                                                                                                      Score 51; DB 2
Pred. No. 4.1;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Encoded by AAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE20521 standard; Protein; 593 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 9B; 50pp; English.
                                                                                                                                                                                                                                                                                                                                      73.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2001; 2001US-0880842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     970S-0863079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7-
Best Local Similarity 67.7-
Frame 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 PDAKTQCPDDST 12
                                                                                                                                                                                                                   altered GP88 activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-267529/31.
N-PSDB; AAD32850.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SERR/) SERRERO G.
                                                                                                                                                                                                                                                                             593 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antineoplastic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2002025543-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAY-1997;
08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serrero G;
                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE20521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A STANDAR STAN
888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dermatological; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antianglogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions.
aspirate, cerebrospinal fluid, liver, kidney, breast, bone, brain, lung, colon, or skin cancer. The method can be used to treat or prevent re-occurrence of cancer in a patient, by administering tamoxifen if the sample contains less than 10 % GPB8, or less than 5 % GPB8 positive cells. The present sequence is human granulin/epithelin precursor (GPB8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis; cytostatic; prolliferative; vulnerary; immunomodulator; antidibabetic; antishmatic; antichematic; antiathritic; antidiral; antidibabetic; antidatritic; antidiral; antidibamatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antianglogemic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; all disorder; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC77607 to AAC78448 encode the human cancer associated proteins given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antithyroid; antiallergic; antibacterial; antiviral;
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer -
                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                                                                                                                          Score 51; DB 23; Length 593; Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cancer associated gene; cancer antigen; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cancer associated protein sequence SEQ ID NO:1416.
                                                                                                                                                                                                                                                                                                                                  Pred. No. 4.1;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 2094-2096; 2352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB43971 standard; Protein; 621 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                              73.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAR-2000; 2000WO-US05882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0124270.
                                                                                                                                                                                                                                                         Query Match
Query Match
Best Local Similarity 66./*,
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1||:::||| ||
209 PDARSRCPDGST 220
                                                                                                                                                                                                                                                                                                                                                                                                                         1 PDÁKTOCPDDST 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-587533/55.
N-PSDB; AAC78180.
                                                                                                                                                                                                                                  593 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200055350-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB43971;
                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                         protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB43971
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us-09-824-647-4.rag

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protein
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            disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate haemostatic or thrombolytic activity, modulate haemostatic or thrombolytic activity, modulate noters, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of the present invention.
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
inhibiting the proliferation, differentiation or mobilisation of nume cells, to treat disorders of haematopoietic cells, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The granulin inhibits keratinocytes and is useful in formulations for promoting the healing of wounds. This peptide was designated granulin F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                 Granulin; keratinocytes; wound healing; inhibition; peptide;
                                                                                                                   Score 51; DB 21; Length 621;
Pred. No. 4.3;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New cystine rich granulin peptide(s) from leucocyte(s) – an
keratinocyte inhibitors useful topically for wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches . 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW01792 standard; Protein; 565 AA.
                                                                                                                                                                                                                                  AAR41886 standard; peptide; 57 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Page 34; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.3%;
58.3%;
                                                                                                                      73.9%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                          92WO-CA00089.
                                                                                                                                                                                                                                                                                                                                                                                                                              92US-0829233.
                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 62.3
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                          111:::||| ||
237 PDARSRCPDGST 248
                                                                                                                             Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                            granulocytes; leucocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 PDSQFECPDFST 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 PDAKTQCPDDST 12
                                                                                                                                                              1 PDAKTQCPDDST 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1993-320328/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SOLO/) SOLOMON S.
                                                                                                    621 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 AA;
 or inhibitions immune cells,
                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                Homo saplens.
                                                                                                                                                                                                                                                                                                                                                                                                                             03-FEB-1992;
                                                                                                                                                                                                                                                                          22-APR-1994
                                                                                                                                                                                                                                                                                                                                                                  W09315195-A.
                                                                                                                                                                                                                                                                                                                                                                                      05-AUG-1993.
                                                                                                                                                                                                                                                                                               Granulin F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Solomon S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                   Sequence
                                                                                                                                                                                                                                                      AAR41886;
                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
                                                                                                                                                                                                               RESULT 12
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                                                                                                                                                                                                                        AAR41886
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SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents the CNK1 protein kinase derived from rat. The gene encoding this sequence is homologous to CDC7 which originates from a mammalian and controls the cell cycle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNK1 gene encodes polypeptide with protein kinase activity - is homologous to Saccharomyces cerevisiae CDC7 cell cycle regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                Protein kinase; enzymatic; Saccharomyces cerevisiae; CDC7; 🖟
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 18; Length 565;
Pred. No. 1.7e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes immunogenic protein #22508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dermatological; osteopathic; neuroprotectant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU61612 standard; Protein; 121 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 6; 9pp; Japanese.
                                                                                                                                                                             cell cycle regulatory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SHKJ ) SHINGLJUTSU JIGYODAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.4%;
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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                                                                                                                                                                                                                                                                                                                                                                                   95JP-0138152
                                                                                                                                                                                                                                                                                                                                                                                                                                   95JP-0138152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-FEB-2002 (first entry)
                                          30-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1: |:|| :|
375 PEVLTKCPDQTT 386
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Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 PDAKTQCPDDST 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Propionibacterium acnes
                                                                                                Rat CNK1 protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-081085/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  565 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAT59400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200181581-A2.
                                                                                                                                                                                                                              Rattus rattus
                                                                                                                                                                                                                                                                   JP08322571-A.
                                                                                                                                                                                                                                                                                                                                                                                   05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUN-1995;
                                                                                                                                                                                                                                                                                                                              10-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU61612;
AAW01792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by the treatment, prevention and diagnosis of medical conditions caused by the treatment, prevention and diagnosis of medical conditions caused by practicals, hypertosis and osteomyelitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory cannows system, however it is particularly involved in the inflammatory sample with a blinding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The can blinding agent that binds to the production of antibodies and determining the amount of bound protein in the sample. The collypeptides may be used as antigens in the production of antibodies of therefore treat P. acnes proteins: These antibodies can be used to downregulate expression and activity of P. acnes pripeptides and ctherefore treat P. acnes infections: The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by contine the sequence data for this patent did not form part of the printed specification, but was obtained in alectronic format directly from WIPPO CC at fitp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                            Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                         Bhatia A;
                                                    Mitcham JL, Wang SS,
Jen S, Carter D;
                                                                                                                                                                                                                                                                                                            Example 1; SEQ ID No 22807; 1069pp; English.
                                            Skeiky YAW, Persing DH, M
L'maisonneuve J, Zhang Y,
                                                                                                                                                                                                                                                                   treating acne vulgaris
(CORI-) CORIXA CORP.
                                                                                                                            WPI; 2001-616774/71
N-PSDB; AAS59619.
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                     Score 40; DB 22; Length 121;
Pred. No. 47;
2; Mismatches 2; Indels
                                              2; Indels
                      58.0%;
                                Local Similarity 60.0
nes 6; Conservative
                                                                    1 PDAKTQCPDD 10
121 AA;
Sequence
                       Query Match
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Propionibacterium acnes immunogenic protein #2956
                         AAU42060 standard; Protein; 323 AA.
                                           27-FEB-2002 (first entry)
| |: :||||
PGARRCPDD 77
   68
                                  AAU42060;
                RESULT 15
                    셤
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SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA, inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant. SAPHO syruveltis;

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Propionibacterium acnes
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WO200181581-A2.

20-APR-2001; 2001WO-US12865 01-NOV-2001

2000US-199047P. 2000US-208841P. 2000US-216747P. 21-APR-2000; 02-JUN-2000; 07-JUL-2000;

(CORI-) CORIXA CORP

Bhatia A; Mitcham JL, Wang SS, , Jen S, Carter D; Persing DH, M e J, Zhang Y, L'maisonneuve J, YAW, Skeiky

WPI; 2001-616774/71. N-PSDB; AAS59516.

Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating ache vulgaris -

SEQ ID No 3255; 1069pp; English. Claim 3;

polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by the treatment, prevention and diagnosis of medical conditions caused by pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. scnes is also involved in infections of bone, joints and the central controls system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention of and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to convergulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

323 AA Seguence

Gaps ö Length 323; Indels Score 39; DB 22; L Pred. No. 1.9e+02; 3; Mismatches 3; 56.5%; 50.0%; Ouery Match
Best Local Similarity 50.v.
Best Local 6; Conservative

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1 PDAKTQCPDDST 12 |: : |||||: PEPQLGCPDDSS 50 ð g completed: July 8, 2003, 16:24:14 : 31 secs Search co

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 8, 2003, 16:21:00 ; Search time 7.38462 Seconds (without alignments) 47.812 Million cell updates/sec Run on:

US-09-824-647-4 69

1 PDAKTQCPDDST 12 Title: ' Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

262574 seqs, 29422922 residues Searched:

262574 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Issued_Patents_AA:*
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 /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*

/cgn2_6/ptodata/1/laa/6A_COMB.pep:* /cgn2_6/ptodata/1/laa/6B_COMB.pep:* /cgn2_6/ptodata/1/laa/PcTUS_COMB.pep:* /cgn2_6/ptodata/1/laa/Packfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

tion	se 4, Appli	'n	9	'n	9		7	6,0	ก่อก	ก่อำกั	ย์กักย์ก	4,000,00	4,0,0,0,4,4	4440000	4446	44440	40440	40440444444	0,000,00,00,00	U0UU0444U4U488	000000000000000000000000000000000000000	000000000000000000000000000000000000000	000000444U40400000	000000444U404888880000	0000044414048888000 80000	000004441404088888000000000000000000000	000004441404888888000000000000000000000
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ID	US-08-991-862-4	US-07-668-648-2	US-07-668-648-6	US-08-429-998-2	US-08-429-998-6	US-08-431-333-	US-08-431-333-6	US-08-991-862-	PCT-US91-02321		PCT-US91-02321	PCT-US91-02321 US-07-668-648-	PCT-US91-02321- US-07-668-648-4 US-08-429-998-4	PCT-US91-02321- US-07-668-648-4 US-08-429-998-4 US-08-431-333-4	PCT-US91-02321 US-07-668-648- US-08-429-998- US-08-431-333- US-08-991-862-	PCT-US91-02321 US-07-668-648- US-08-429-998- US-08-431-333- US-08-991-862- PCT-US91-02321	PCT-US91-02321 US-07-668-648- US-08-429-998- US-08-431-333- US-08-991-862- PCT-US91-02321 US-08-336-891-	PCT-US91-02321- US-07-668-648-4 US-08-429-998-4 US-08-991-862-1 PCT-US91-02321- PCT-US95-13795-	PCT-US91-02321- US-07-668-648-4 US-08-429-998-4 US-08-991-862-1 PCT-US91-02321- US-08-336-891-2 PCT-US95-137395- US-07-668-648-8	PCT-US91-02321- US-07-668-648-4 US-08-431-333-4 US-08-991-862-1 US-08-991-862-1 US-08-991-862-1 US-08-991-862-1 US-08-336-891-8 US-07-668-648-8 US-08-429-998-8	PCT-US91-02321- US-07-668-648-4 US-08-431-333-4 US-08-991-862-1 US-08-991-862-1 US-08-991-862-1 US-08-991-895-13795- US-07-668-648-8 US-07-668-648-8 US-08-429-998-8	PCT-0591-02321 US-08-648-648- US-08-429-393- US-08-991-862- PCT-US91-02331 PCT-US93-13795- US-08-68-648- US-08-431-333- US-08-431-333- PCT-US91-13133-	PCT-US91-02321-03231-03231-03231-03231-03231-03231-03231-03231-03231-03231-03231-03231-03231-03-08-431-33-8	PCT - US91 - 02321 - 6 US - 07 - 668 - 648 - 4 US - 08 - 429 - 98 - 4 US - 08 - 431 - 33 - 4 US - 08 - 991 - 862 - 17 PCT - US91 - 02321 - 4 US - 08 - 336 - 891 - 2 US - 08 - 336 - 891 - 2 US - 08 - 429 - 998 - 8 US - 08 - 429 - 998 - 8 US - 08 - 431 - 333 - 8 US - 08 - 431 - 333 - 8 US - US91 - 02321 - 8 US - US91 - 02321 - 8 US - US9 - 233 - 989 - 5 US - 09 - 233 - 989 - 5	PCT-US91-02321 US-07-668-648- US-08-421-933- US-08-431-333- US-08-991-862- PCT-US91-02321 US-08-38-891- US-08-429-998- US-08-429-998- US-08-421-333- US-08-431-333- US-08-431-333- US-09-233-989- US-09-233-989- US-09-564-805- US-09-564-805-	PCT-US91-02321-0321-0321-0321-0321-0321-0321-03	PCT-US91-02321 US-08-431-333- US-08-431-333- US-08-991-862- US-08-991-862- PCT-US91-02321 US-08-36-891-862- US-08-31-333- US-08-431-333- US-08-431-333- US-09-233-989- US-09-240-2454 US-09-540-2454 US-09-540-2454
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Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0		100.0	100.0	100.0 73.9 73.9	100.0 73.9 73.9 73.9	100.0 73.9 73.9 73.9 73.9	100.0 73.9 73.9 73.9 73.9	100.0 73.9 73.9 73.9 73.9 73.9 55.1	100.0 73.9 73.9 73.9 73.9 73.9 55.1	100.0 73.9 73.9 73.9 73.9 73.9 55.1 55.1	100.0 73.9 73.9 73.9 73.9 55.1 55.1 53.6	100.0 73.9 73.9 73.9 73.9 73.9 73.9 73.6 53.6 53.6 53.6	100.0 73.9 73.9 73.9 73.9 73.9 73.9 53.6 53.6 53.6 53.6	100 7 7 7 3 3 3 9 9 9 9 9 9 9 9 9 9 9 9 9 9	100 733 733 733 733 733 733 733 733 733 7	100 733 733 733 733 733 733 733 733 733 7	1000 77330 5830 58	100.0 73.9 73.9 73.9 73.9 73.9 73.9 73.9 73.9
Score	69	69	69	69	69	69	69	69	69		69	69 51	69 51 51	51 51 51	51 51 51 51	69 51 51 51 51	69 51 51 51 51 38	69 51 51 51 51 38 38	69 51 51 51 51 51 38 38	69 51 51 51 51 51 51 38 38 37	69 51 51 51 51 51 83 33 37 37	69 51 51 51 51 31 32 37	69 51 51 51 51 31 32 37 37 37 37	69 51 51 51 33 37 37 36 36	69 511 511 31 31 31 31 31 31 31 31	69 511 511 33 33 34 36 36	69 5511 5511 37 37 38 38 38 38 38
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28	36	52.2	1480	2	PCT-US91-09055-2	Sequence 2, Appli	
29	35.5	51.4	35	~	US-08-190-802A-220	Sequence 220, App	
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36	35.5	51.4	488	7	US-08-487-072A-60	60,	
37	35	50.7	388	7	US-08-742-621-1	Sequence 1, Appl1	
38	32	50.7	388	4	US-09-191-608-22	Sequence 22, Appl	
39	35	50.7	407	7	US-08-742-440A-3	e,	
40	35	50.7	529	٣	US-08-821-984-6	9	
41	32	7.05	529	٣	US-08-821-984-8	Sequence 8, Appli	
42	35	50.7	529	4	US-09-329-749-6	9	
43	35	50.7	529	4	US-09-329-749-8	Sequence 8, Appl1	
44	35	50.7	809	Н	US-07-789-915A-4	Sequence 4, Appli	
45	35	50.7	809		US-08-005-002C-4	Sequence 4, Appli	
		4					
		_÷*			ALIGNMENTS		
		s.f	,				
RESULT 1			/				
US-08-991-862-4	1-862-4						
: Sednen	ce 4, A	\pplicat	Sequence 4, Application US/08991862	680	91862		
; Patent	Patent No. 6309826	Patent No. 6309826					
10000	-						

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; LOCATION: (1)...(12)
; OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the ; OTHER INFORMATION: antisera against the GP88 used in the ; OTHER INFORMATION: immunoaffinity step.
APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996-488/P001-A
GURRENT APPLICATION NUMBER: US/08/991,862
CURRENT FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/863,862
EARLIER APPLICATION NUMBER: 09/05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PALENTIN VAI. 2.0
                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: mouse granulin
                                                                                                                                                                                                                                                      SEQ ID NO 4
LENGTH: 12
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Length 12; 0; Indels 100.0%; Score 69; DB 4; 100.0%; Pred. No. 1e-05; Live 0; Mismatches 0 Local Similarity 100. nes 12; Conservative Query Match Best Loc Matches

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Gaps

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Sequence 2, Application US/07668648 Patent No. 5416192 GENERAL INFORMATION: 1 PDAKTQCPDDST 12 1 PDAKTQCPDDST 12 US-07-668-648-2 RESULT 2 g ò

ENEKAL ARE SLOYAD, MOHARMEU
APPLICANT: Shoyab, MOHARMEU
APPLICANT: PLOWAR, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROFEINS CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas

STATE:

Gaps

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Indels

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APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
                                                              Length 589;
                                                                                                                                                                                                                                                                                                                                                                                                            NOVEL CYSTEINE-RICH GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 69; DB 2; 100.0%; Pred. No. 0.0007;
                                                            Query Match 100.0%; Score 69; DB 1; Best Local Similarity 100.0%; Pred. No. 0.0007, Matches 12; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Shoyab, Mohammed
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYST
TITLE OF INVENTION: MODILATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEDE: Pennie, & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,998
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIGH APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08429998 Patent No. 5885961 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08429998
Patent No. 5885961
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION TELEPHONE: (212)790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212) 869-9741 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 589 amino acids
amino acid
                                                                                                                                                                                           208 PDAKTQCPDDST 219
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                   1 PDAKTOCPDDST 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
; MOLECULE TYPE: protein US-07-668-648-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-429-998-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
                                                                                                                                                                                                                                                                             JS-08-429-998-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS-08-429-998-6
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Patent No. 5416192
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
Plowman, Gregory D.
TITLE OF INVENTION:
MODILATING PROTEINS
NUMBER SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie 6 Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 69; DB 1; Length 589;
Pred. No. 0.0007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION UNDER: US/07/668,648
FILING DATE: 19910819
                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,648
FILING DATE: 19910819
                                                                                                                                                                                                        CIASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
TELEFHONE: (212) 869-9741
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Pennie & Edmonds
STREET: 1155 Ayenue of the Americas
                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION UNDERST: 18,872
REFERENCE/DOCKET UNDERST: 56
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212,790-909)
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                : 589 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 589 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 PDAKTQCPDDST 219
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Best Local Similarity 100.
Matches 12; Conservative
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                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York
: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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Length 589;
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                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 69; DB 2; Best Local Similarity 100.0%; Pred. No. 0.0007; Matches 12; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                             NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Shoyab, Mohammed
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL C'
TITLE OF INVENTION: MODULATING PROFEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 27-APR-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/431,333
FILING DATE: 27-APR-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08431333
Patent No. 5965723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                       100.0%;
100.0%;
                                                                                                               TELEPHONE: (212)790-9090
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Misrock, S. Leslie
              ATTORNEY/AGENT INFORMATION NAME: Misrock, S. Leslie
                                                                                                                                                                                               LENGTH: 589 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 869-9741 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                        MOLECULE TYPE: protein US-08-431-333-2
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Sequence 2, Application US/08431333

Patent No. 5965723

GENERAL INFORMATION:
APPLICANT: Showman, Gregory D.
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 589;
                                                                                                                                                                                                                                                 OPERATION SYSTEM: PC-LUSS/RS-LUSS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,998
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATORNEY/AGNT INFORMATION:
NAME: MISTOCK: S. LESIE
REGISCOMUNICATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
TELEPHONE: (212)790-9090
TELEPHONE: (212)790-9090
TELEPHONE: (212) 869-9741
INPORMATION FRO IN OIC 6:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 69; DB 2;
Pred. No. 0.0007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSEE: Pennie & Edmonds
EET: 1155 Avenue of the Americas
: New York
7: New York
7: USA
100.0
MODULATING PROTEINS
12
                                                      ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
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                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-429-998-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                  COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 12; Conserva
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Length 589;

DB 5;

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ID, GREGOLY D.

H: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH

H: MODULATING PROTEINS

S: 12
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                       0.0007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
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Pred. No. 0.0007;
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                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Bristol-Myers Squibb Company
STREET: 3005, First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CY
TITLE OF INVENTION: MODULATING PROTEINS
                 Score 69;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: POOT, BIAIN W. 22,928
RECISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: 0N0071A-PC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                        Sequence 6, Application PC/TUS9102321
Sequence 6, Application PC/TUS9102321
Sequence 5, Shoyab, Mohammed
APPLICANT: Shoyab, Mohammed
TITLE OF INVENTION: EPITHELINS: NOVE
TITLE OF INVENTION: MODULATING PROFE
TUTLE OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02321
FILING DATE: 19910403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-07-668-648-4; Sequence 4, Application US/07668648; Patent No. 5416192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
                   100.0%;
100.0%;
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
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                                                                                                                 208 PDAKTQCPDDST 219
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208 PDAKTQCPDDST 219
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                                                          Conservative
                                                                                          1 PDAKTQCPDDST 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 PDAKTOCPDDST 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein PCT-US91-02321-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie 6 F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 Query Match
Best Local Similarity 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 12; Conserva
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CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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PCT-US91-02321-6
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TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/08/991,862
CURRENT FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/863,862
BARLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: BPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
CORRESPONDENCE: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 69; DB 4; Length 589; 100.0%; Pred. No. 0.0007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICAMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Bristol-Myers Squibb Company
STREET: 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19910403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application PC/TUS9102321 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Mouse epithelin/granulin
US-08-991-862-2
                                                                                                                                 Sequence 2, Application US/08991862
Patent No. 6309826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: ON TELECOMMUNICATION: TELEPHONE: (206)728-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 589 amino acids
AMINO ACID
(206)448-4775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1111111111
208 PDAKTQCPDDST 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 PDAKTOCPDDST 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein PCT-US91-02321-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
FILING DATE: 199104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
STATE: Washington
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                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                            RESULT 8
US-08-991-862-2
                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 589
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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Length 589;

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                                                                                                                           Length 593; 🕸
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APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: MODILATING PROTEINS
TITLE OF INVENTION: MODILATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 593;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,333
FILING DATE: 27-APR-1995
CLASSIFICATION: 536
CLASSIFICATION DATA:
APPLICATION NUMBER: US/0/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                               DB 2;
                                                                                                                                               Pred. No. 0.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
                                                                                                                             Score 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 17, Application US/08991862; Patent No. 6309826
                                                                                                                                                                                                                                                                                                                         US-08-431-333-4; Sequence 4, Application US/08431333; Patent No. 5965723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pennie & Edmonds
                                                                                                                               73.9%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: amino acid
               : 593 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 869-9741 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111:::111 | 11
209 PDARSRCPDGST 220
                                                                                                                                                                                                                                 209 PDARSRCPDGST 220
                                                                                                               Query Match
Best Local Similarity 66.7.
8; Conservative
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Best Local Similarity 66.7
Matches 8; Conservative
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SEQUENCE CHARACTERISTICS:
LENGIH: 593 amino acid
                                                                                                                                                                                                           1 PDAKTQCPDDST 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-431-333-4
                                         ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-429-998-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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US-08-991-862-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 593
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MEDIUM TYPE: Floppy disk
COMPUTER: TBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,998
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,648
FILING DATE: 19910819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 51; DB Pred. No. 0.7;
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APPLICATION NUMBER: US 07/668,648

FILING DATE: 13-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: MISTOCK, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 5624-161-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4 Application US/08429998
Patent No. 588561
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION:
FITLE OF INVENTION: MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                           CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624
TELECHONE: (212)790-9090
TELEFAN: (212) 869-9741
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66./*,
Best Local Similarity 61./*,
Best Local Similarity 61./*,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212) 869-9741 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                          : 593 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209 PDARSRCPDGST 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 PDAKTQCPDDST 12
                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
   New York
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
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   STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-668-648-4
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us-09-824-647-4.rai

GENERAL INFORMATION:

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Search completed: July 8, 2003, 16:30:18
Job time: 9.38462 secs
APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: 08/08/991.862
CURRENT APPLICATION NUMBER: 08/863,862
EARLIER APPLICATION NUMBER: 08/863,862
EARLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 17
LENGTH: 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Shoyab, Mohammed
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5; Length 593;
                                                                                                                                                                                                                                                                                                                                                DB 4; Length 593;
                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02321
FILING DATE: 19910403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company
STREET: 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0071A-PC
FELECOMMUNICATION INFORMATION:
TELEPHONE: (206)728-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
PCT-US91-02321-4
; Sequence 4, Application PC/TUS9102321
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                Query Match 73.9%;
Best Local Similarity 66.7%;
Matches 8; Conservative
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NAME: POOR, Brian W
REGISTRATION NUMBER: 32,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 PDAKTOCPDDST 12
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209 PDARSRCPDGST 220
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209 PDARSRCPDGST 220
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Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                               ; ORGANISM: Human GP88 cDNA
US-08-991-862-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-02321-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : Seattle
3: Washington
FRY: USA
98121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                             PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ptodata/2/pubpaa/US07_FUBCOMB.pep
ptodata/2/pubpaa/US08_NEW_PUB.pep
ptodata/2/pubpaa/US08_PUBCOMB.pep
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                  445758 seqs, 116419773 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                   - protein search, using sw model
                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                            US-09-824-647-4
69
1 PDAKTQCPDDST 12
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                           Sequence:
                                                                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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/ptodata/2/pubpaa/US09_PUBCOMB.pep: /ptodata/2/pubpaa/US10_NEW_PUB.pep:

'pubpaa/US09_NEW_PUB.pep

SUMMARIES

Description	Sequence 4, Appli	Sequence 4, Appli	~ `	Sequence 4, Appl1	4	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 17, Appl	Sequence 17, Appl	Sequence 17, Appl	Sequence 17, Appl	Sequence 17, Appl	Sequence 1416, Ap	Sequence 44137, A	Sequence 129, App	Sequence 37818, A
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OI EC	9 US-09-824-647-4	9 US-10-218-509-4	9 US-10-281-160-4	10 US-09-813-156-4	10 US-09-824-807-4	9 US-09-824-647-2	9 US-10-218-509-2	9 US-10-281-160-2	10 US-09-813-156-2	10 US-09-824-807-2	9 US-09-824-647-17	9 US-10-218-509-17	9 US-10-281-160-17	10 US-09-813-156-17	10 US-09-824-807-17	10 US-09-925-301-1416	10. US-09-864-761-44137	10 US-09-789-561-129	10 US-09-864-761-37818
H.	2	2	2	2	2	39	. 66	39	39	39	33	33	33	593	33	21	37	94	398
Query Match Length DB	0.00	0.00	0.00	0.00	0.00		0.001			0.00.		73.9 5	73.9 5	73.9 5	73.9 5	73.9 6.	55.1	55.1	53.6 3
;	-	_	_	-	_	_	_	_	_	_	_	_	_	_	_	_	_	<u>~</u>	~
Score	59	59	59	9	69	59	69	59	59		51	51	51	51	51	51	36	36	'n
Result No.	-		m	4	5	9	7	8	Q	10.	11	12	13	14	15	16	17	18	19

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Sequence 4, Application US/10218509 Publication No. US20030092661A1 GENERAL INFORMATION:

US-10-218-509-4

RESULT

Sequence 145, App Sequence 4, Appl1 Sequence 4, Appl1 Sequence 11, Appl Sequence 11, Appl Sequence 4, Appl1 Sequence 4, Appl1 Sequence 4, Appl Sequence 448, App Sequence 448,	11, A 448, 448, 448, 448,
0. US-10-133-128-145 0. US-09-864-761-37187 US-10-000-157-4 US-10-000-157-4 US-10-036-041-11 US-09-320-713-29 US-09-320-713-29 US-09-320-713-29 US-09-747-259-4 US-10-175-737-448 US-10-175-737-448 US-10-175-737-448 US-10-175-738-448 US-10-175-738-448 US-10-175-738-448 US-10-175-738-448 US-10-176-482-448 US-10-176-482-448 US-10-176-482-448 US-10-176-938-448 US-10-176-938-448 US-10-176-938-448 US-10-176-938-448 US-10-176-938-448 US-10-176-938-448 US-10-176-938-448	US-09-931-836-11 US-10-173-700-448 US-10-174-572-448 US-10-174-579-448 US-10-174-589-448 US-10-174-588-448
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ALIGNMENTS

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US-09-824-647-4

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US-09-824-647-4

US-09-824-647-4

Sequence 4, Application US/09824647

Publication No. US20020183270A1

GENERAL INFORMATION:

APPLICART: Serieso', Ginette

APPLICART: Serieso', Ginette

TITLE OF INVENTION: 88 KDA TUMORISENIC GROWTH FACTOR AND ANTAGONISTS

FILE OF INVENTION: 88 KDA TUMOLA-64

CURRENT APPLICATION NUMBER: DS/01-04-04

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,862

PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23

PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 4

LENGTH: 1.2

TYPE: PRT

ORGANISM: mouse granulin

FRATORE:

NAME/KEY: PEPTIDE:

LOCATION: (1)...(12)

OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the OTHER INFORMATION: Immunoaffinity step.

UCCATION: (1)...(12)

OUTHER INFORMATION: Immunoaffinity step.

US-09-824-647-4

QUECY WATCH

NAME OF SEQ ID NOS: 17

ORGANISM: MOUSE GRANTING: MINIMATCHES 0; Indels 0; Gaps

ON 1 PDAKTQCPDDST 12

DD 1 PDAKTQCPDDST 12

DD 1 PDAKTQCPDDST 12
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APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REPERENCE: 299964.484/POLICA
CURRENT APPLICATION NUMBER: US/09/813,156
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1997-12-16
PRIOR FILING DATE: 1997-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29964.484/POL1-A
CURRENT APPLICATION NUMBER: US/09/824,807
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR PPLICATION NUMBER: 08/991,862
PRIOR PLICATION NUMBER: 08/963,862
PRIOR FILING DATE: 1997-12-16
PRIOR FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCATION: (1). (12)
OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the OTHER INFORMATION: antisera against the GP88 used in the OTHER INFORMATION: immunoaffinity step.
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100.0%; Pred. No. 4e-05;
ive 0; Mismatches 0;
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Patent No. US20020094966al
GENERAL INFORMATION:
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; Sequence 2, Application US/09824647
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
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Best Local Similarity 100.
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
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Best Local Similarity 100.
Matches 12; Conservative
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## APPLICANT: Serrero, Ginette
### TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
### FILE REPERENCE: 29996.488 / FOOL-A
### CURRENT APPLICATION NUMBER: 08/510/218,509
### CURRENT FILING DATE: 2002-08-15
### FROR APPLICATION NUMBER: 08/991,862
### FROR PELION DATE: 1998-08-17
### FROR FILING DATE: 1998-08-17
### FROR FILING DATE: 1998-08-17
### FROR FILING DATE: 1997-05-23
### ROAP FILING DATE: 1997-05-33
### FROR FILING DATE: 1997-06-33
### FROR FILING DATE: 1998-08-17
### FROR FILING DATE: 1998-08-1
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TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: Z9996.488/P001-A
CURRENT APPLICATION NUMBER: US/10/281,160
CURRENT FILING DATE: 2002-10-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)...(12)
OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the OTHER INFORMATION: antisera against the GP88 used in the OTHER INFORMATION: immunoaffinity step.
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OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the OTHER INFORMATION: antisera against the GP88 used in the OTHER INFORMATION: immunoaffinity step.
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Pred. No. 4e-05;
0; Mismatches 0; Indels
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PRIOR FILING DATE: 1998-08-17
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PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFFWARE: Patentin Ver. 2.0
SEQ ID NO 4
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GENERAL INFORMATION:
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Matches 12; Conservative
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Best Local Similarity
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US-09-813-156-4
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Gaps

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NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 3
                                                                LENGTH: 58
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                                             SEQ ID NO 2
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Publication No. US20030092661A1
GENERAL INFORMATION:
APPLICAMT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE APPLICATION NUMBER: US/10/218,509
CURRENT APPLICATION NUMBER: US/10/218,509
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR APPLICATION NUMBER: 08/963,862
                                     APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/09/824,647
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17
PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23
NUMBER: OF SEQ ID NOS: 17
SOFTWARE: PATENTING DATE: 1997-05-23
LENGTHRE: 589
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Publication No. US20030108950A1
GENERAL: INFORMATION:
APPLICANT: Seriero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001.A
CURRENT APPLICATION NUMBER: US/10/281,160
CURRENT FILING DATE: 2002-10-28
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Pred. No. 0.0021;
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PRIOR FILING DATE: 1998-08-17
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                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Mouse epithelin/granulin
US-09-824-647-2
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US-10-218-509-2
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100.0%;
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NUMEBR OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 589
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Best Local Similarity 100.

Matches 12; Conservative
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Patent No. US20020094966al
RENEMATION:
APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/09/824,807
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 08/991,862
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Serrero, Ginette TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS FILE REFERENCE: 29996.488/P001-A CURRENT APPLICATION NUMBER: US/09/813,156 CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                Query Match , 100.0%; Score 69; DB 9; L Best Local Similarity 100.0%; Pred. No. 0.0021; Matches 12; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 0.0021;
:ive 0; Mismatches 0;
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PRIOR FILING DATE: 1997-12-16
PRIOR PAPLICATION NUMBER: 08/863,862
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 2
LENGTH: 589
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PRIOR APPLICATION NUMBER: 08/863,862
PRIOR FILING DATE: 1997-05-23
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                                                                                   ; ORGANISM: Mouse epithelin/granulin US-10-281-160-2
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 589
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Patentin Ver. 2.0
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Best Local Similarity 100.
Matches 12; Conservative
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APPLICANT: Serrero, Ginette
TITLE OF INFWATION:
FILE REFERENCE: 29996.488/P001-A
CURRENT FILIAG DATE: 201-03-21
PRIOR APPLICATION NUMBER: US/09/813,156
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR PILING DATE: 1997-12-16
PRIOR PILING DATE: 1997-12-16
PRIOR PILING DATE: 1997-12-16
PRIOR PILING DATE: 1997-05-23
PRIOR PILING DATE: 1997-05-23
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Patent No. US20020094966A1
GENERAL INFORMATION:
APPLICANT: SETIECO, GINETTE
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REPERBENC: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/09/824,807
CURRENT FILING DATE: 2001-04-04
APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/10/281,160
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: US/08/991,862
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: U8/863,862
PRIOR FILING DATE: 1997-05-23
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Pred. No. 1.8;
3; Mismatches
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Pred. No. 1.8;
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PRIOR PLICATION NUMBER: 08/991,862
PRIOR PLILING DATE: 1997-12-16
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NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
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SEQ ID NO 17
LENGTH: 593
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Best Local Similarity 66.7
Matches 8; Conservative
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; ORGANISM: Human GP88 CDNA
US-10-281-160-17
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APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 2996.488/P001-A
CURRENT APPLICATION NUMBER: US/10/218,509
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-23
                                                                                                                                                                       Sequence 17, Application US/09824647
Publication No. US20020183270A1
GENERAL INFORMATION:
Publication No. US20020183270A1
GENERAL INFORMATION:
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REPERRENC: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/09/824,647
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,862
PRIOR PILING DATE: EARLIER FILING DATE: 1998-08-17
PRIOR PILING DATE: EARLIER FILING DATE: 1998-08-17
PRIOR PILING DATE: EARLIER FILING DATE: 1997-05-23
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Pred. No. 1.8;
3; Mismatches 1; Indels
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Pred. No. 1.8;
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Publication No. US20030092661A1
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Best Local Similarity 66.7%;
Matches 8; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 593
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 593
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209 PDARSRCPDGST 220
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US-10-218-509-17
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Matches 8; Conservative
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US-09-824-647-17
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RESULT 13

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us-09-824-647-4 rapb
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; SEQ ID NO 17 ; LENGTH: 593 ; TYPE: PR: ; ORGANISM: Human GP88 CDNA US-09-824-807-17

0; Gaps Query Match
73.9%; Score 51; DB 10; Length 593;
Best Local Similarity 66.7%; Pred. No. 1.8;
Matches 8; Conservative 3; Mismatches 1; Indels

1 PDAKTQCPDDST 12 |||:::||| || 209 PDARSRCPDGST 220

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Search completed: July 8, 2003, 16:31:40 Job time: 12.6923 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.
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July 8, 2003, 16:19:45; Search time 12.1538 Seconds (without alignments) 94.918 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-09-824-647-4 69 1 PDAKTQCPDDST 12 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	epithelin/granulin	epithelin/granulin	acrogranin - guine	granulin precursor	protein T22H2.6 [1	hypothetical prote	hypothetical prote	סי	exo-beta-D-fructos	ribonuclease TRV (hypothetical prote	hypothetical prote	hypothetical prote	growth modulatory	iron-dependent rep	transcription regu	transcription regu	bile acid-inducibl	, variant surface gl	peptidase M13 fami		hypothetical prote		hypothetical prote		myoblast determina	transcription regu	alpha-D-mannose-al	probable membrane
DI	C38128	B38128	148141	GYHU	E87929	T25138	T25137	AC3545	A49206	JX0197	T33366	T16381	н97712	A46654	C84211	AG1436	AH1078	E69371	S18447	F87683	T28812	AH2701	T32698	T35736	C96691	A29636	A87388	H83985	АН0728
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% Query Match	100.0	100.0	81.2	73.9	62.3	62.3	62.3	6.09	58.0	57.2	56.5	56.5	56.5	55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	53.6		•	٠	53.6	53.6	53.6	53.6
Score	69	69	99	51	43	43	43	42	40	39.5	39	39	39.	38	38	38	, 38	38	38	38	38	37	37	37	37	37	37	37	37
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Gaps ; 0

Length 589;

Query Match 100.0%; Score 69; DB 2; Length 58
.Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels

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RESULT 2 B38128

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53.6	53.6	53.6	53.6	53.6	53.6	53.6	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	
37	37	37	37	37	37	37	36	36.	36	36	36	36	36	36	36	
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ALIGNMENTS

RESULT 1

C; pate: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 20-Aug-1999 C; pate: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 20-Aug-1999 C; Accession: C38128; S32603; I49468; A46705 R; Plowman, G. D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Tod J. Biol. Chem. 267, 13073-13078, 1991 A; Title: The epitthelin precursor encodes two proteins with opposing activities on A; Reference number: A38128; MUD:92317004; PMID:1618805 A; Accession: C38128 A; Molecule type: mRNA A; Residues: 1-589 - CPLO> A; Cross references: GB:X62321; NID:950851; PIDN:CAA44197.1; PID:950852 R; Babb, T.; Momoto, H.; Matenabe, K.; Arai, Y.; Gerton, G.L. FEBS Lett. 322, 89-94, 1993 A; Title: Exon/Intron organization of the gene encoding the mouse epithelin/granu A; Reference number: S32503; MUD:93245991; PMID:8482392 A; Title: Exon/Intron organization of the gene encoding the precusor of A; Residues: 18-349, L.; 351-589 - CBB> B; Babb, T.; Hoff, H.B. A; Residues: 18-349, L.; 351-589 - CBB> B; Babb, T.; Hoff, H.B. A; Residues: 18-349, L.; 351-589 - CBB> A; Title: Acrogranin, an acrosomal cysteine-rich glycoprotein, is the precusor of A; Reference number: 148461 A; Molecule type: mRNA A; Residues: 1-250, L', 252-233, V', 255-349, L', 351-401, SA', 404-589 - RES> A; Cross-references: GB:M86736; NID:93226926; PMID:84A37191.1; PID:9191767 B; Diol. Chem. 268, 10863-10869, 1993 A; Title: Purification of an autocrime growth factor homologous with mouse epithe A; Reference number: A46705; MUID:9326626; PMID:84496151 A; Reterence number: Pathinianry A; Retues: preliminary	A; Molecule type: protein A; Residues: 18-19, 'X', 21-25, 'X', 27-29, 'XX', 32; 'XXX', 119-127; 152-154, 'DXK', 158-16		C. Superfamily: granulin
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N;Alternate names: epithelin
N;Contains: granulin A; granulin B; granulin C; granulin D; granulin E; granulin F;
C;Species: Homo saptens (man)
C;Date: 30-Sep-1992 #sequence_revision 03-May-1996 #text_change 08-Dec-2000
C;Date: 30-Sep-1992 #sequence_revision 03-May-1996 #text_change 08-Dec-2000
C;Date: 30-Sep-1992 #sequence_revision 03-May-1996 #text_change 08-Dec-2000
C;Accession: JC1284; A38128; A38118; A36698; B36698; C36698; D36698; A56873
R;Bhandari, V.; Bateman, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plowman, G.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Todard. Blockler, 267, 13073-13078, 1992. Tille: The epithelin precursor encodes two proteins with opposing activities on effectence number: A38128; MUID:92317004; PMID:1618805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross references: GB:X62320; NID:931192; PIDN:CAA44196.1; PID:931193; Bhandari, V.; Palfree, R.G.E.; Bateman, A. roc. Natl. Acad. Sci. U.S.A. 89, 1715-1719, 1992; Fitle: Isolation and sequence of the granulin precursor cDNA from human bone marrafeference number: A38118; MUID:92179253; PMID:1542665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: mRNA
Residues: 1406, K7,408-433,'G',435-453,'G',455-459,'Q',461-546,'A',548-566,'R',:
Cross-references: GB:M/5161; NID:9183612; PIDN:AAA58617.1; PID:9183613
Note: this sequence has been revised in reference JC1284
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A;Introns: 46/3; 88/3; 117/1; 154/3; 200/1; 236/3; 279/1; 311/3; 393/3; 471/3; 548,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title: Characterisation of UGP and its relationship with beta-core fragment. Reference number: A56873; MUID:93229246; PMID:8471426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. Biophys. Res. Commun. 188, 57-63, 1992
A;Title: Structure and chromosomal location of the human granulin gene.
A;Reference number: JC1284; MUID:93038704; PMID:1417868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ď
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Accession: B36698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bateman, A.; Belcourt, D.; Bennett, H.; Lazure, C.; Solomon, ochem Biophys. Res. Commun. 173, 1161-1168, 1990
Title: Granulins, a novel class of peptide from leukocytes. Reference number: A36698; MUID:91097544; PMID:2268320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: protein
Residues: 442-446, XDTSS',456-458,'DG' <BA4>
Kardana, A.; Bagshawe, K.D.; Coles, B.; Read, D.; Taylor, M.
F. J. Cancer 67, 686-692, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: sequence extracted from NCBI backbone (NCBIP:129524)
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Residues: 206-218, H',220-233 <BA2>
Note: this protein was purified and characterized as
Accession: C36698
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Residues: 364-367,/X',369-385,'H',387-396 <BA3>
NOte: this protein was purified and characterized as
Accession: D36698
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A.Residues: 281-283,'X',285-289,'S',291-295 <KAR>
A.Experimental source: urine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GDB:136006; OMIM:138945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Superfamily: granulin
C; Keywords: glycoprotein; tandem repeat
                                                                                                                                                                                              - human
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Residues: 281-336 <BAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-593 <BHA>
3; Plowman, G.D.; Green,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Residues: 1-593 <PLO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: A38128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: JC1284
epithelin/granulin precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 20-Aug-1999
C;Accession: B38128; A36199; E36698; 153272
R;Plowman, G.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Todaro, G.J.
J, Biol. Chem. 267, 13073-13078, 1992
A;Title: The epithelin precursor encodes two proteins with opposing activities on epithe
A;Reference number: A38128; MUID:92317004; PMID:1618805
A;Molecule type: mRNA
A;Ressidues: 1-589 <PID>
A;Ressidues: 1-589 <PID>
A;Ressidues: 1-589 <PID>
A;Residues: 1-580 <PID>
A;Residues: 280-300 <PID
A;Res
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c;Species: Cavia porcellus (guinea pig)

c;Species: Cavia porcellus (guinea pig)

c;Accession: 148141

c;Accession: 148141

c;Accession: 148141

Nol. Reprod. Dev. 34, 233-243, 1993

A;Title: Acrogranin, an acrosomal cysteine-rich glycoprotein, is the precusor of the grd

A;Reference number: 148141

A;Reference number: 148141

A;Reference number: 148141

A;Reference number: 148141

A;Reference number: 158141

A;Residues: 1-591 cRBS

A;Residues: 1-591 cRBS

A;Residues: 1-591 cRBS

A;Cross-references: GB:M86735; NID:g191234; PIDN:AAA37030.1; PID:g191235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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R; Bhandari, V; Giaid, A.; Bateman, A.
Endocrinology 133, 268-2689, 1993
A; Title: The complementary decoxyribonucleic acid sequence, tissue distrib
A; Reference number: 153272; MUID: 94062640; PMID: 8243292
A; Accession: 153272
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-200, 'S', 203-388, 'M', 390-589 <RES>
A; Cross-references: GB: M97750; NID: 9204223; PIDN: AAA16903.1; PID: 9204224
C; Superfamily: granulin
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A; Residues: 205-226 <SH2>
R; Bateman, A; Belcourt, D.; Bennett, H.; Lazure, C.; Solomon, Biochem. Biophys. Res. Commun. 173, 1161-1168, 1990
A; Title: Granulins, a novel class of peptide from leukocytes. A; Reference number: A36698; MOID:91097544; PMID:2268320
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100.0%; Pred. No. 0.0011;
""" """ "" "" Indels
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Pred. No. 0.15;
4; Mismatches
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Fresidues: 279-307, SB', 310-324,'T',32
Bhandari, V:; Giaid, A: Bateman, A.
Adocrinology 133, 2682-2689, 1993
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66.7%;
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Best Local Similarity 66.7
Matches 8; Conservative
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Matches 12; Conserva
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F;18-593/Product: granulin #status predicted <MAT> F;18-593/Product: progranulin #status predicted <PRO>

11:::|||||:| 209 PDSRSOCPDDIT 220

1 PDAKTQCPDDST 12

9 9

Domain: signal sequence #status predicted

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Ribelvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; I.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D. proc. Natl. Acad. Sci. US.A. 99, 443-448, 2002
A;fitle: The genome sequence of the facultative intracellular pathogen Brucella A;Reference number: AD3252; PMID:11756688
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C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A49206
R;Burne, R.A.; Penders, J.E.
Infect. Immun. 60, 4631-4632, 1992
A;Title: Characterization of the Streptococcus mutans GS-5 fruA gene encoding ex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              periplasmic dipeptide transport protein precursor BMEI10284 [imported] - Brucell:
                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:281595; PIDN:CAB54304.1; GSPDB:GN00019; CESP:T22H2.6a
A;Experimental source: clone T22H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE008918; PIDN:AAL53526.1; PID:g17984432; GSPDB:GN00191
A;Experimental source: strain 16M
                                                                                                                                                                                            C;Species: Caenorhabditis elegans
C;Bate: 15-Oct-1999 %sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T25137
R;Lennard, N.
submitted to the EMBL Data Library, November 1996
A;Reference number: 219985
A;Reference number: 219985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AC3545
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                                                                                                                                                                       - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 7
Pred. No. 13;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 62.3
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: 1
A; Introns: 93/3; 232/3; 314/3
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Les 7; Conservative
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                                                                                                                                                                       hypothetical protein T22H2.6a
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| DAETECSDDET 109
                                              99 DAETECSDDET 109
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  2 DAKTQCPDDST
                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-358 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-506 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: CESP: T22H2.6a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: AC3545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: BMEI10284
A; Map position: II
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Best Local S
Matches 7
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A:Note: see websites genome wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross - references: GB: chr_I; PIDN: CAB04752.1; PID: 93880056; GSPDB: GN00019; CESP: T22H2.
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A;Experimental source: clone T22H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T25138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein T22H2.6 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: E87929
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                                              F;123-179/Product: granulin F #status predicted <GRF>
F;206-261/Product: granulin B #status experimental <GRB>
F;208-136/Product: granulin A #status experimental <GRA>
F;364-417/Product: granulin C #status experimental <GRC>
F;442-496/Product: granulin D #status predicted <GRD>
F;318-573/Product: granulin E #status predicted <GRE>
F;318-573/Product: granulin E #status predicted <GRE>
F;368/Binding site: carbohydrate (Asn) (covalent) #status experimental
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#status experimental <= 
#status predicted <GRG>
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A;Molecule type: DNA
A;Residues: 1-345 <WIL>
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Pred. No. 12;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; anonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, November 1996
A; Reference number: Z19985
A; Accession: T25138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
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Pred. No.
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ilarity 63.6%;
Conservative
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Best Local Similarity 66.7%;
Matches 8; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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A; Introns: 93/3; 232/3; 314/3
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Best Local Similarity
Matches 7; Conserv
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A; Molecule type: DNA
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A;Gene: pntB
C;Superfamily: NAD(P)+ transhydrogenase (B-specific) beta chain; NAD(P)+ transhydrc
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A'Residues: 1-222 <LEI>
A'Cross-references: EMBL:U39646; NID:g1049351; PID:g1049353; PIDN:AAA80368.1; CESP:
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C; Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 10-Nov-1995
C; Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 10-Nov-1995
C; Accession: A46654; A40180
R; Belcourt, D.R.; Lazure, C.; Bennett, H.P.
A; Biol. Chem. 268, 9230-9237, 1993
A; Title: Isolation and primary structure of the three major forms of granulin-like
A; Reference number: A46654; MUID:93252781; PMID:8486624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: H97712
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093, 2009, 2001
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893
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A;Molecule type: DNA
A;Residues: 1.465 <KUR>
A;Cross-references: GB:AE006914; PIDN:AAL02642.1; PID:915619144; GSPDB:GN00173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein pntB [imported] - Rickettsla conorii (strain Malish 7)
C;Species: Rickettsla conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
                                                                                                                                                                            ).Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: CESP:F47B7,4
A;Introns: 81/3; 97/1; 116/1; 163/3; 212/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F16G10.4
                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, October 1995
A;Description: The sequence of C. elegans cosmid F47B7
A;Reference number: 218504
A;Accession: T16381
                                                                                                                         - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB 2;
Pred. No. 72;
2; Mismatches
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nilarity 66.7%;
Conservative 2
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291 AKTSCPEDA :299
                                                                                                                            ypothetical protein F47B7.
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Best Local Similarity
6; Conserve
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A; Residues: 1-57 <BEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: H97712
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R; Leimbach, D.
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C; Species: Trichoderma viride
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: JX0197
R; Inada, Y; Watanabe, H.; Ohgi, K.; Irie, M.
J. Blochem. 110, 896-904, 1991
A; Filte: Isolation, characterization, and primary structure of a base non-specific and A; Reference number: JX0197; MUID:92176163; PMID:1794979
A; Recession: JX0197
A; Molecule type: protein
A; Residues: 1-234 <IMD.
C; Superfamily: Enterbacter ribonuclease
C; Superfamily: Briterbacter ribonuclease
C; Keywords: glycoprotein; hydrolase
C; Keywords: glycoprotein; hydrolase
F;15/Binding site: carbohydrate (Asn) (covalent)
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Cispecies: caenorhabditis elegans
Cispecies: 29-oct-1999 #text_change 20-Jun-2000
Cistudy, S.; Scheet, P.
Submitted to the EMBL Data Library, July 1998
A; Description: The sequence of C. elegans cosmid F16G10.
A; Reference number: 221329
A; Reference number: 221329
A; Recession: T3356
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Rolecule type: DNA
A; Residues: 1-190 <GAT>
A; Residues: 1-190 <GAT>
A; Residues: 1-190 <GAT>
A; Cross references: EMBL:AF077537; PIDN:AAC26282.1; GSPDB:GN00020; CESP:F16G10.1
A; Experimental source: strain Bristol N2; clone F16G10
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C.Species: Caenorhabditis elegans
C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000
A; Reference number: A49206; MUID:93014178; PMID:1398976
A; Contents: GS-5
A; Accession: A49206
A; Atcession: A49206
A; Atcession: A49206
A; Atcession: A49206
A; Anolecule type: nucleic acid
A; Molecule type: nucleic acid
A; Residues: 1-1423 ABMA-
A; Residues: 1-1423 ABMA-
A; Cross-references: GB:L03358; NID:94733888; PIDN:AAA26889.1; PID:9153634
A; Note: sequence extracted from NCBI backbone (NCBIN:116439, NCBIP:116440)
                                                                                                                                                                                                                                                                                                                                   Gaps
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A;Introns: 61/3; 84/1; 127/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F16G10.4
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Pred. No. 1.4e+02;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ribonuclease TRV (EC 3.1.27.-) - fungus (Trichoderma viride)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39.5; DE Pred. No. 32; 1; Mismatches
                                                                                                                                                                                                                                                              58.0%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 57.2%;
Best Local Similarity 72.7%;
Matches 8; Conservative
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Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                 Query Match 58.0
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 PD-AKTQCPDD 10
|| ||: ||||
217 PDGAKSTCPDD 227
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PTSTTKCPDLST 80
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619 PDLHTECPD 627
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Gene: CESP:F16G10.1
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JX0197
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Gaps

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Indels

Length 222;

DB 37;

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Gaps ö

Indels

Length 465;

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C; Accession: C84211

R; Ng, W.V.; Kennedy, S.P.; Mahalras, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jable Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Authors: Bou, S.; Daniels, C.J.; Dennis, P.P.; Omcr. A.D.; Ebhardt, H.; Lowe, T.M.; Li A; Reference number: A84160; MUID: 20504483; PMID: 11016950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-144 <STO>
A;Cross-references: GB:AE004437; NID:g10580129; PIDN:AAG19055.1; GSPDB:GN00138
                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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A;Note: sequence extracted from NCBI backbone (NCBIP:131314)
C;Comment: All twelve Cys residues are involved in disulfide bonds.
C;Reywords: disulfide bond; monomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 2; Length 144;
Pred. No. 36;
1; Mismatches 1; Indels
                                                                                                   Score 38; DB 2; Length 57;
Pred. No. 16;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                           1ron-dependent repressor [imported] - Halobacterlum sp. NRC-1
C.Species: Halobacterium sp. NRC-1
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Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                      Query Match 55.1%;
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                       5 DAATICPDGTT 15
                                                                                                                                                                                                            2 DAKTQCPDDST 12
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Search completed: July 8, 2003, 16:29:25 Job time : 15.1538 secs

| |:|||| 116 DRKSQCPD 123

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

July 8, 2003, 16:16:30; Search time 5.84615 Seconds (without alignments) 85.136 Million cell updates/sec Run on:

US-09-824-647-4 69 1 PDAKTQCPDDST 12

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892'seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ption	r granulins	mus musculu	cavia porce	h granulins	mus musculu	streptococc	trichoderma	cyprinus ca	trypanosoma	vesicular s	cucumper mo	mus musculu	homo sapten	homo sapten	homo sapten	mus musculu	homo sapien	homo sapien	sus scrofa	mycoplasma	cryphonectr	homo sapten	saccharomyc	schizosacch	drosophila	escherichia	saccharomyc	rickettsia	mus musculu	phanerochae	homo sapien	homo sapien	saccharomyc
Description	P23785	P28798	P28797	P28799	0920h0	003174	P24657	P81013	P26327	P04884	083270	P10085	P35658	999600	P22105	09j1c3	09p0m4	P15172	P49811	P47631	000548	000311	P38830	010197	P24014	P27862	P33750	Q9zca0	008675	P50622	099571	P49747	P25037
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	GRN_RAT	GRN_MOUSE	GRN_CAVPO	IN_HUMAN	CDC7_MOUSE	FRUA_STRMU	RNTR_TRIVI	GRN1_CYPCA	VSI2_TRYBB	VGLG_VSVO	VIA_CMVII	MYOD_MOUSE	N214_HUMAN	AHNK_HUMAN	TENX_HUMAN	SELX_MOUSE	117C_HUMAN	MYOD_HUMAN	MYOD_PIG	AMPA_MYCGE	SUX1_CRYPA	CDC7_HUMAN	NDT8_YEAST	ALP1_SCHPO	SLIT_DROME	YIGZ_ECOLI	SOF1_YEAST	Y866_RICPR	PAR3_MOUSE	LIG6_PHACH	P2X4_HUMAN	COMP_HUMAN	JBP1_YEAST
8	GR.	GR	GR	GRN	5	FR	Z	5	Ν	Š	5	Ä	NZ	AH	TE	SE	11	¥	¥	Ş	9	5	Z	ΑĽ	SI	Y	SC	ΧB	PA	3	2	8	5
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Query Match Length	588	289	. 591	593	564	1423	234	. 57	479	511	993	318	2090	2960	4289	116	197	319	319	447	452	574	627	1121	1480	204	489	107	369	372	388	757	808
Query Match	100.0	100.0	81.2	73.9	59.4	58.0	57.2	55.1	55.1	55.1	55.1	53.6	53.6	53.6	53.6	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	51.4	51.4	50.7	50.7	50.7	50.7	50:7	50.7
Score	69	69	26	51	41	40	39.5	38	38	38	38	37	37	37	37	36	36	36	36	36	36	36	36	36	36	35.5	35.5	32	32	32	35	35	35
Result No.	-	7	m	₹.	'n	9	7	80	σ	10	11	12	13	. 14	15	16	17	18	19	20	21	22	23	. 24	25	56	27	28	. 29	30	31	32	33

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schizosacch	drosophila	mus musculu	mus musculu	ophiophagus	aipysurus l	scenedesmus	cyanophora	saccharomyc	vibrio chol	haemophilus	vaccinia vi	
P40848	P25992	P01029	004592	P01412	P19960	P00238	P17007	004307	09km76	P44101	P21090	
DHP1_SCHPO	YEMA_DROME	CO4_MOUSE	PCK5_MOUSE	TXW1_OPHHA	NXS4_AIPLA	FER_SCEOU	FER1_CYAPA	RPCZ_YEAST	NRDG_VIBCH	YA43_HAEIN	VC23_VACCC	
-		-	П	-	Н	Н	Н	7	-	-	-	
991	1002	1738	1877	09	81	96	86	110	155	166	244	
50.7	50.7	50.7	50.7	49.3	49.3	49.3	49.3	49.3	49.3	49.3	49.3	
35	35	35	35	34	34	34.	34	34	34	34	34	
34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Granulins precursor (corpusin) [Contains: Granulin 1; Granulin 2; Granulin 3; Granulin 4; Granulin 5; Granulin 6; Granulin 7].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plowman G.D., Green I.M., Neubauer M.G., Buckley S., McDonald V.L., Todaro G.I., Shoyab M.;

The epithelin precursor encodes two proteins with opposing activities on epithelial cell growth.";

J. Biol. Chem. 267:13073-13078(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
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MEDLINE-93245991; PubMed-8482392;
Baba T., Nemoto H., Watanabe K., Arai Y., Gerton G.L.;
"Exon/intron organization of the gene encoding the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113D434F7E099B31 CRC64;
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N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
S -> FP (IN REF. 2).
TK -> SB (IN REF. 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q -> T (IN REF. 4).
M -> I (IN REF. 2).
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FEBS Lett. 322:89-94(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       589 AA.
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GRANDLIN 5.
GRANDLIN 6.
GRANDLIN 7.
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                                                                                                                                                                                                                                                                                                                                                                      PS00799; GRANULINS; 7. Repeat; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                      InterPro; IPR000118; Granulin.
Pfam; PF00396; granulin; 7.
SMART; SM00277; GRAN; 7.
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                                                                                                                                                           EMBL; M97750; AAA16903.1; -. EMBL; X62322; CAA44198.1; -.
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Best Local Similarity 100.

Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                   GRAN; 7
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PIR; B36199; B36199
PIR; E36698; E36698.
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P28798;
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                                                                                                                                                                                                                                                                                                                                             SMART; SM
PROSITE;
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
-i- FUNCTION: GRANULINS HAVE POSSIBLE CYTOKINE-LIKE ACTIVITY. THEY MAY PLAT A ROLE IN INTELAMMATION, WOUND REPAIR, AND TISSUE REMODELING.
-i- TISSUE SPECIFICITY: UBIQUITOUS.
-i- PTM: GRANULINS ARE DISULFIDE BRIDGED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOL. Reprod. Dev. 34:233-243(1993).
-!- FUNCTION: GRANULINS HAVE POSSIBLE CYTOKINE-LIKE ACTIVITY. THEY MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Acrogranin, an acrosomal cysteine-rich glycoprotein, is the precursor of the growth-modulating peptides, granulins, and epithelins, and is expressed in somatic as well as male germ cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cavia porcellus (Guinea pig).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Granulins precursor (Acrogranin) [Contains: Granulin 1; Granulin 5; Granulin 7]
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..) (POTENTIAL).
..) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 69; DB 1; I
Pred. No. 0.00043;
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1DE8229C413CB787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GLCNAC
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SEQUENCE FROM N.A., AND SEQUENCE OF 4-21.
                                                                                                                                                                                                                                                                                                                                ACROGRANIN.
GRANULIN 1.
GRANULIN 3.
GRANULIN 4.
GRANULIN 5.
GRANULIN 6.
GRANULIN 6.
N-LINKED (G.
N-LINKED (G.
N-LINKED (G.
                                                                                                                                                                                                                                                                                                     Signal
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                                                                                                                                                                                                                                                                                                     Glycoprotein;
                                                                                                                                                                                                                                                                                  PROSITE; PS00799; GRANULINS; 7. Cytokine; Repeat; Glycoprotein:
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                                                                                                                                                                                                                            MGD; MGI:95832; Grn.
InterPro; IPR000118; Granulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63458 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.08;
                                                                                                                                                                                EMBL; D16195; BAA03736.1; -. FMBL: M86736; AAA37191.1; -.
                                                                                                                                                                                                EMBL; M86736; AAA37191.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.08;
                                                                                                                                                                                                                                                        Pfam; PF00396; granulin; 7. SMART; SM00277; GRAN; 7.
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208 PDAKTQCPDDST 219
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Best Local Similarity
Local 12; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    589 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Fragment).
GRN.
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P28797:
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MEDLINE=92317004; PubMed=1618805;
                                                                                                                                              TISSUE-Brain;
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 138945;
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P28799; P23781; P23782; P23784; Q9BWE7;
O1-NOV-1991 (Rel. 20, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 24, Last sequence update)
Granulins precursor (Acrogranin) [Contains: Paragranulin; Granulin 1 (Granulin G); Granulin 2 (Granulin F); Granulin 3 (Granulin B);
Granulin 4 (Granulin A); Granulin 5 (Granulin C); Granulin 6 (Granulin D); Granulin 7 (Granulin E)].
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 WOUND REPAIR, AND TISSUE REMODELING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Structure and chromosomal location of the human granulin gene."; nochem. Biophys. Res. Commun. 188:57-63(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -LINKED (GLCNAC. . .) (POTENTIAL). EE7C9FC8F21CB8A1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bhandari V., Palfree R.G.E., Bateman A.;
"Isolation and sequence of the granulin precursor cDNA from bone marrow reveals tradem cysteine-rich granulin domains.";
Proc. Natl. Acad. Sci. U.S.A. 89:1715-1719(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 56; DB 1; Length 591;
Pred. No. 0.058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
PLAY A ROLE IN INFLAMMATION, WOUND RE
1- TISSUE SPECIFICITY: UBIQUITOUS.
1- PTM: GRANULINS ARE DISULFIDE BRIDGED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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GRANULIN 4.
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GRANULIN 6.
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GRANULIN 2.
                                                                                                                                                                                                                                                                                                                                                                                ACROGRANIN
                                                                                                                                                                                                                                                                                                                     Repeat; Signal; Glycoprotein.
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MEDLINE-92179253; PubMed=1542665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS, SEQUENCE FROM N.A. MEDLINE-93038704; Pubmed-1417868;
                                                                                                                                                                                                                                       InterPro; IPR000118; Granulin. Pfan; PF00396; Granulin; 7. SMART; SW00277; GRAN; 6. PROSITE; PS00799; GRANULINS; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62586 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.28;
                                                                                                                                                                                                                      EMBL; M86735; AAA37030.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 PDSRSQCPDDTT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 66.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                          591
798
7164
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2494
2569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           439
7518
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                                                                                                                                                                                                                                                                                                                  Cytokine; F
NON_TER
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Plowman G.D., Green I.M., Neubauer M.G., Buckley S.D., McDonald V.L., Todaro G.J., Shoyab M.; The epithelin precursor encodes two proteins with opposing activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bateman A., Belcourt D.R., Bennett H.P., Lazure C., Solomon S., "Granulins, a hovel class of peptide from leukocytes."; Biochem. Biophys. Res. Commun. 173:1161-1168(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: GRANULIAN HAVE FUSSIBLE LITUALINE-LIKE ACTIVITY. THEY MAY PLAY A ROLE IN INFLAMMATION, WOUND REPAIR, AND TISSUE REMODELING.

-!- FUNCTION: GRANULIN A PROMOTES PROLIFERATION OF THE EPITHELIAL

CELL LINE A431 IN CULTURE WHILE GRANULIN B ACTS AS AN ANTAGONIST
TO GRANULIN A, INHIBITING THE GROWTH.

-!- GRANULIN A, INHIBITING THE GROWTH.

-!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be produced by alternative splicing.

-!- TISSUE SPECIFICITY: IN MYELOGENOUS LEUKEMIC CELL LINES OF PROMONOCYTIC, PROMYELOCYTIC, AND PRORYTHROID LINEAGE, IN FERSENT IN INFLAMMATORY CELLS AND BONE MARROW. HIGHEST LEVELS IN KIDNEY.

-!- PTW: GRANULINS ARE DISULFIDE BRIDGED.
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(POTENTIAL).
(POTENTIAL).
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Pfam; PF00396; granulin; 7.
SMART; SMOG377; GRAN; 7.
PROSITE; PS00799; GRANULINS; 7.
Cytokine; Repeat; Glycoprotein; Signal; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                      Iu W., Glbbs R.A.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 206-233; 281-336; 364-396 AND 442-447
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GRANULIN 6.
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N-LINKED
                                                                                                                                                                                                                                                                                                                                                                      (ISOFORMS 1 AND 2)
                                                                                               on epithelial cell growth.";
J. Biol. Chem. 267:13073-13078(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M75161; AAA58617.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Leukocyte;
MEDLINE-91097544; PubMed-2268320;
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EMBL; AROSOOB; AACO359.1; -.
EMBL; BC000324; AARH00334.1; -.
EMBL; BC010577; AAH10577.1; -.
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOF) TISSUE-Cervix, and Lung;
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2573
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PIR; D36698; D36698.
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                                                                                                                                                                                                         SEQUENCE FROM N.A.
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DR KW KW CFT FFT SO

62752 MW;

SEQUENCE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kim J., Sato N., Yamada M., Arai K., Masai H.;
"Growth regulation of the expression of mouse cDNA and gene encoding a serine/threonine kinase related to Saccharomyces cerevisiae CDC7 essential for GI/S transition. Structure, chromosomal localization, and expression of mouse gene for s. cerevisiae Cdc7-related kinase."; J. Biol. Chem. 273:23248-23257(1998).

- FUNCTION: SEDAS TO PHOSEPHORYLATE CRITICAL SUBSTRATES THAT REGULATE THE GI/S PHASE TRANSITION AND/OR DNA REPLICATION. CAN
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLUIAR LOCATION: Nuclear (By similarity).
ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARE PRODUCED BY ALTERNATIVE SPLICING. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                       CDC7_MOUSE STANDARD; PRT; 504 AA.
GDC7_20010 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation concernation update)
16-OCT-20010 (Rel. 40, Last annotation update)
16-OCT-20010 (Rel. 40, Last annotation update)
N-LINKED (GLCNAC. .).
N-LINKED (GLCNAC. .) (POTENTIAL).
MISSING (IN ISOFORM 2).
G -> 0.
                                                                                                                                                                       ö
                                                                                                                                     Score 51; DB 1; Length 593;
Pred. No. 0.38;
                                                                                                                                                                       1; Indels
                                                                                                          4E402BDB16DE2819 CRC64;
                                                           /FTId=VAR_003445.
S -> H (IN REF. 6).
W -> H (IN REF. 6).
                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOINED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98389757; PubMed-9722556;
                                                                                                          63473 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB019388; BAA34347.1; -
EMBL; AB019378; BAA34347.1; JG
                                                                                                                                     73.9%;
66.7%;
                                                                                                                         Query Match
Best Local Similarity 66.7°
                                                                                                                                                                                                                     109 PDARSRCPDGST 220
                                                                                                                                                                                                   1 PDAKTQCPDDST 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BAA34347
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                          386
593 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDC7 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:1309511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                        CDC7L1 OR CDC7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Liver
                                                                                            CONFLICT
CARBOHYD
CARBOHYD
                              VARSPLIC
                                                                           CONFLICT
                                             VARIANT
                                                                                                                                                                                                                                                                                             CDC7_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
EMBL;
EMBL;
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                                                                                                                                                                                                                                                                               RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burne R.A., Penders J.E.C.; "Characterization of the Streptococcus mutans GS-5 fruA gene encoding exo-beta-D-fructosidase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR INVERTASE.
-!-CATALITIC ACTIVITY: Hydrolysis of terminal-non-reducing 2,1- and 2,6-linked beta-D-fructofuranose residues in fructans.
-!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (Potential).
-!- INDUCTION: BY SUCRASE, FRUCTAN SUBSTRATES AND FRUCTOSE.
-!- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Infect. Immun. 60:4621-4632(1992).
-1- FUNCTION: THIS PROFEIN IS A FRUCTANASE ENZYME WHICH DEGRADES
-1- EVANS AND INULING TO FRUCTOSE AND ALSO CLEAVES SUCROSE INTO
GLUCOSE AND FRUCTOSE AND CAN THEREFORE FUNCTION AS AN
                                                                                            ;
0
                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Fructan beta-fructosidase precursor (EC 3.2.1.80) (Exo-beta-D-
                                                 Score 41; DB 1; Length 564;
                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
MISSING (IN ISOFORM 2).
925791D5F93FBA02 CRC64;
                                                                                          3; Mismatches
                                                                      Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003343; B1g_2.
InterPro; IPR001362; GH_32.
InterPro; IPR01899; Gram_pos_anchor.
Pfam; PF00251; Glyco_hydro_32; 1.
Pfam; PF02368; B1g_2; 1.
IIGRFAMS; IIGR01167; LPXTG_anchor; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93014178; PubMed-1398976;
                                                      59.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U78296; AAA26889.1; -.
                                                                                                                                                                                                                                                                                                                                                                       fructosidase) (Fructanase)
                                                                                                                                                   1: |:|| :|
373 PEVLTKCPDOTT 384
                                                                                          6; Conservative
                                                                                                                                1 PDAKTQCPDDST 12
                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus mutans.
                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-1309;
                                                                                                                                                                                                                                                          FRUA_STRMU
Q03174;
                                                      Query Match
                                                                                                                                                                                                                                          FRUA_STRMU
                                                                                            Matches
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. A SOLUBLE FORM IS RELASED FROM RUPTURED CELLS BY THE ACTION OF A
                                                                                                                                                                            Bukaryota: Metazoa; Chordata; Craniata; Vortebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostarlophysi; Cypriniformes;
Cyprinidae; Cyprinus.
NCBI_TaxID=7962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. MOI. BIOL. 221:823-835(1991).
-1- FUNCTION: VSG FORMS A COAT ON THE SURFACE OF THE PARASITE. THE
TYPANOSOME EVADES THE IMMURE RESPONSE OF THE HOST BY EXPRESSING
A SERIES OF ANTIGENICALLY DISTINCT VSGS FROM AN ESTIMATED 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Variant specific glycoprotein of Trypanosoma brucei consists of tw
domains each having an independently conserved pattern of cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Isolate MIAG 202B;
MEDLINE-92046037; PubMed-1942032;
Carrington M., Miller N., Blum M.L., Roditi I., Wiley D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB 1; Length 57;
Pred. No. 5.6;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Variant surface glycoprotein ILTAT 1.22 precursor (VSG).
                                                                                                                                                                                                                                                                                                                                                                                                                                              E4A131B1288FE55A CRC64;
                                                                                                           (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 35, Last annotation update)
                                                                                    57 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              479 AA.
                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000118; Granulin.
Pfam; PF00396; granulin; 1.
SMART; SM00277; GRAN; 1.
                                                                                                                                                                Cyprinus carpio (Common carp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.1%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               6289 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trypanosoma brucei brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 63.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                        217 PDGAKSTCPDD 227
                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 DAKTQCPDDST 12
1 PD-AKTQCPDD 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                57 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSG GENES.
                                                                                                           01-NOV-1997
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Turner M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSI2_TRYBB
P26327;
                                                                                                                                                    Granulin 1
                                                                                     GRN1_CYPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 residues.
                                                                                                                                                                                                                                           SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytokine
                                                                                                   P81013;
                                                             RESULT 8
GRN1_CYPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSI2_TRYBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92176163; PubMed-1794979;
MEDLINE-92176163; PubMed-1794979;
Inada Y., Watanabe H., Ohgi K., ITie M.;
Isolation, characterization, and primary structure of a base non-specific and adenylic acid preferential ribonuclease with higher specific activity from Trichoderma viride.";
J. Blochem. 110:896-904(1991).
PREFERENTIAL RIBONUCLEASE.
                       e; Cell wall; Peptidodlycan anchor; Signal.
POTENTIAL.

REMOTENTIAL.

REMOTED BY SORTASE (POTENTIAL).

BY SIMILARITY

INVOLVED IN BINDING OF SUGARS WITH
BETA-(2,6) LINKRAGES OR BINDING OF
MOLECULAR WEIGHT FRUCTANS (BY
                                                                                                                                      LPXTG SORTING SIGNAL (POTENTIAL).
AMIDE-LINKED TO CELL WALL (POTENTIAL).
MW; 8E574715F4E72A8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- CATALYTIC ACTIVITY: Two-stage endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphacligonucleotides with 2',3'-cyclic phosphate intermediates.
-1- SIMILARITY: BELONGS TO THE RNASE T2 FAMILY.
                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ribonuclease Trv (EC 3.1.27.1) (RNASE Trv).
Trichoderma viride.
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Trichoderma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 234;
                                                                                                                                                                                         DB 1; Length 1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8B011DD65A3F909A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .).
 GLYCOSYL_HYDROL_F32; FALSE_NEG. GRAM_POS_ANCHORING; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mydrolase; Nuclease; Endonuclease; Glycoprotein.
                                                                                                                                                                                        Score 40; DB 1
Pred. No. 56;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                  234 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39.5;
                                                                                                                            SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001568; RNase_T2.
Pada; PF00445; Inbonuclease_T2; 1.
PROSITE; PS00530; RNASE_T2_1; 1.
PROSITE; PS00531; RNASE_T2_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 N-75 N-25901 MW;
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                                                                                                                                      1388 1392
1391 1391
1423 AA; 158668
                                                                                                                                                                                         58.0%;
66.7%;
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                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                  STANDARD;
                           Glycosidase;
                                                 1391
1423
458
871
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619 PDLHTECPD 627
                                                                                                                                                                                                                                          1 PDAKTQCPD 9
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Matches 8; Conserv
                                                                                                                                                                                                    Best Local Similarity
Matches 6; Conserv
 PS00609;
                                                                                                                                                                                                                                                                                                                               RNTR_TRIVI
P24657;
             PROSITE; PS:
Hydrolase; (
                                                                                                                                                                                                                  .;
9
                                                 CHAIN
PROPEP
ACT_SITE
DOMAIN
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SEQUENCE
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 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
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                                                                                                                                                                                          Query Match
                                    SIGNAL
                                                                                                                                                                                                                                                                                                                   RNTR_TRIVI
                                                                                                                                        SITE
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Gaps

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consists of two

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MYOD_MOUSE
P10085;
01-MAR-1989 (
01-MAR-1989 (
15-DEC-1998 (
                                                                                                                                                                                                                                                                                                                                                                     Cucumovirus
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9
  CARBOHYD
CARBOHYD
                                                                       SEQUENCE
                              VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
MYOD_MOUSE
    FFFFFS
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                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bioinformatics and the EMEL outstation the European Hoinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91/YOPDTOTELL.";
J. VITOL. 54:374-382(1985).
I. VITOL. 54:374-382(1985).
I. VITOL. 54:374-382(1985).
I. VITOL. 54:374-382(1985).
I. SUNTION: THIS PROTEIN FOR THE BINDING OF THE VIRUS TO SUSCEPTIBLE HOST CELLS AND FOR INDCING THE UPTAKE OF THE VIRUS BY THE CELL. THE INTERACTION BETWEEN THE INTERNAL COMPONENTS OF THE VIRION AND THE PORTION OF THE GLYCOPROTEIN EXPOSED ON THE CYTOPLASHIC FACE OF THE PLASMA MEMBRANE PROBABLY DIRECTS ENVELOPMENT AND
                                                                                                                                                                 Glycoprotein; Antigen; Trypanosomiasis; GPI-anchor; Membrane; Signal.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                VARIANT SURFACE GLYCOPROTEIN ILTAT 1.22
                                                                                                                                                                                                            HYDROPHOBIC, REMOVED DURING MATURATION.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE-85185664; PubMed-2985803;
Gallione C.J., Rose J.K.;
Gallione C.J., Rose J.K.;
A single amino acid substitution in a hydrophobic domain causes temperature-sensitive cell-surface transport of a mutant viral
                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                               DB 1; Length 479;
                                                                                                                                                                                                                                                   GPI-ANCHOR (BY SIMILARITY).
FF7205FF0F58435A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vesicular stomatitis virus (strain Orsay).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Rhabdoviridae; Vesiculovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001903; Rhabd_glycop.
Pfam; PF00974; Rhabd_glycop; 1.
Transmembrane; Envelope protein; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPIKE GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
01-JUL-1989 (Rel. 11, Last annotation update)
                                                                                                                                                                                                                                                                                             Score 38; DB 1
Pred. No. 42;
3; Mismatches
                                                                                                                                                                                                                                                                  51457 MW;
                                                                                                                                       EMBL; X56765; CAA40084.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spike glycoprotein precursor
                                                                                                                                                                                                                                                                                                                                                                   1 : :|||: |
263 PSSSNKCPDEGT 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M11048; AAA48438.1;
                                                                                                                                                                                                                                                                                                                         5; Conservative
                                                                                                                                                                                                                                                                                                                                                     1 PDAKTQCPDDST 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                      ; S18447.
                                                                                                                                                                                                                                                                  479 AA;
                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-11284;
                                                                                                                                                    PIR; S18447
                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGLG_VSVO
P04884;
                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                            PROPEP
                                                                                                                                                                                               CHAIN
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VGLG_VSVO
STEPFFFFFFFFFFFFFFF
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
F -> S (IN TEMPERATURE-SENSITIVE
F TSO45, WHICH EXHIBITS TEMPERATURE
-SENSITIVE CELL.SURFACE TRANSPORT).
                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Karasawa A., Ito A., Okada I., Hase S., Ehara Y.;
"A possible role of RNA 2 of cucumber mosalc cucumovirus as a determinant of infection phenotype on cowpea.";
Ann. Phytopathol. Soc. Jpn. 63:289-297(1997).
-!- FUNCTION: MAY BE INVOLVED IN THE REPLICATION OF THE VIRUS.
CONTAINS AN HELICASE DOMAIN AND A METHYLTRANSFERASE DOMAIN. THE METHYLTRANSFERASE DOMAIN. THE METHYLTRANSFERASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Last Sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1A protein [Includes: Helicase; Methyltransferase].
Cucumber mosaic virus (strain lizuka) (CMV).
Viruses; SSRNA positive-strand viruses, no DNA stage; Bromoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                       Length 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: TO 1A PROTEIN FROM BMV, CCMV, PSV AND TAV.
                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01660; Vmethyltransf; 1.
Helicase; ATP-binding; Transferase; Methyltransferase.
NP_BIND 714 721 ATP (POTENTIAL).
SEQUENCE 993 AA; 111479 MW; BCD95906008B1CA7 CRC64;
                                                                                                                                                                                       Score 38; DB 1;
Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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(Rel. 10, Last sequence update)
(Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               993 AA
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                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002588; V.methyltransf.
InterPro; IPR000606; Viral_helicasel.
Pfam; PF01443; Viral_helicasel; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
ID VIA.CMVII
ID VIA.CMVII STANDARD; PRI
AC 083270; Care 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequen
DT 16-OCT-2001 (Rel. 40, Last annote
                                                                                                                                   57570 MW;
                                                                                                                                                                                    55.1%;
63.6%;
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ilarity 54.5%;
Conservative
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                                                                                                                                                                               Query Match
Best Local Similarity 63.6
Matches 7; Conservative
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548 PEASSQTPDDT 558
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336
204
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Best Local Similarity
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DR KWW KWW SOR SO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER BHLH PROTEIN. SEEMS TO FORM ACTIVE HETERODIMERS WITH ITF-2. SUBCELLULAR LOCATION: Nuclear. SIMILARIY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS. "MYOGENIC FACTORS" SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOI. Cell. Biol. 17:6563-6573(1997).
--I-FUNCTION: INVOLVED IN MUSCLE DIFFERENTIATION (MYOGENIC FACTOR).
INDUCES FIBROBLASTS TO DIFFERENTIATE INTO MYOBLASTS. ACTIVATES
MUSCLE-SPECIFIC PROWOTERS. INTERACTS WITH AND IS INHIBITED BY THE
TWIST PROTEIN. THIS INTERACTION PROBABLY INVOLVES THE BASIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98001585; PubMed-9343420;
Hamamori Y., Nu H.Y., Sartorelli V., Kedes L.;
"The basic domain of myogenic basic helix-loop-helix (bHLH) proteins
is the novel target for direct inhibition by another bHLH protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ď
                                                                                                                                                                                                                                                                                                                                                                                                                        *MyoD1: a nuclear phosphoprotein requiring a Myc homology region to convert fibroblasts to myoblasts."; Science 242:405-411(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94236689; PubMed-8181063;
Ma P.C.M., Rould M.A., Weintraub H., Pabo C.O.;
Crystal structure of MyoD bHLH domain-DNA complex: perspectives on DNA recognition and implications for transcriptional activation.";
Cell 77:451-459(1994).
                                                                                                                                                                                                                                                MEDLINE-92093599; PubMed-1754380;
Zingg J.M., Alva G.P., Jost J.P.;
"Characterisation of a genomic clone covering the structural mouse
                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myogenic lineage determination and differentiation: evidence for
                                                                                                                                 MEDLINE-88080485; PubMed-3690668;
Davis R.L., Weintraub H., Lassar A.B.;
*Expression of a single transfected cDNA converts fibroblasts to
                                                                                                                                                                                                                                                                                                                                                                                     Tapscott S.J., Davis R.L., Thayer M.J., Cheng P.-F., Weintraub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pinney D.F., Pearson-White S.H., Konleczny S.F., Latham K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 102-166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                      MyoD1 gene and its promoter region.";
Nucleic Acids Res. 19:6433-6439(1991)
                                                                                                                                                                                                                         MEDLINE-88223371; PubMed-3286015;
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-89019371; PubMed-3175662;
   Myoblast determination protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAINS OF BOTH PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M18779; AAA39799.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulatory gene pathway.";
Cell 53:781-793(1988).
                                                                                                                                                                                                    51:987-1000(1987).
                                   musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INHIBITION BY TWIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                   SEQUENCE FROM N.A.
                 MYOD.
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                                                                                                                                                                                        myoblasts
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                                                                                                                                                                                                                                                                                                                                                         FUNCTION
                 MYOD1
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EMBL; X61655; CAA43836.1; -. EMBL; M84918; AAA39798.1; -.

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Proc. Natl. Acad. Sci. U.S.A. 91:1519-1523(1994).

-!- FUNCTION: MAY SERVE AS A DOCKING SITE IN THE RECEPTOR-MEDIATED

IMPORT OF SUBSTRATES ACROSS THE NUCLEAR PORE COMPLEX.

-!- SUBUNIT: HONODIMER. INTERACTS WITH DDX19.

-!- SUBCELLULAR LOCATION: NUCLEAR PORE COMPLEX. CYTOPLASMIC FILAMENTS.

-!- TISSUE SPECIFICITY: EXPRESSED IN THYMUS, SPLEEN, BONE MARROW,

KIDNEY, BRAIN AND TESTIS, BUT HARDLY IN ALL OTHER TISSUES OR IN

WHOLE EMBRYOS DURING DEVELORMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The translocation (6,9), associated with a specific subtype of acute myeloid leukemia, results in the fusion of two genes, dek and can, and the expression of a chimeric, leukemia-specific dek-can mRNA."; Mol. Cell. Biol. 12:1687-1697(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: PROBABLY GLYCOSYLATED AS IT REACT WITH WHEAT GERM AGGLUTININ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NONLYMPHOCYTIC LEUKEMIA) (AML) CARRYING A CHROMOSOMAL
TRANSLOCATION T(6;9)(P23;034) THAT RESULTS IN THE FORMATION OF A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISEASE: IMPLICATED IN A SUBSET OF ACUTE MYELOID LEUKEMIA (ACUTE
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myeloid leukemogenesis, is a nuclear pore complex protein that faces the cytoplasm.";
                                                                                                                                                                                                                                                    Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                               HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Nuclear pore complex protein Nup214 (Nucleoporin Nup214) (214 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Testis;
MEDILMS-92195315; PubMed-1549122;
Von Lindern M., Fornerod M., Van Baal S., Jaegle M., De Wit T.,
Buljs A., Grosveld G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kraemer D., Wozniak R.W., Blobel G., Radu A.; The human CAN protein, a putative oncogene product associated
                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                     Score 37; DB 1; Length 318
                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                               48C836896FCBDC0C CRC64;
                                                                                                                                                                                                                                                                      Transcription regulation; DNA-binding; 3D-structure.
DNA_BIND 109 121 BASIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                              4;
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                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          42;
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MEDLINE-94151361; PubMed-8108440;
                                                                       MGD; MGI:97275; Myodl.
InterPro: IPR001092546; Basic.
InterPro: IPR001092; HLH_basic.
Pfam; PF0010; HLH; 1.
SMART; SM00520; BASIC; 1.
SMART; SM0053; HLH; 1.
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                                                                                                                                                                                                                                                                                                                                 34218 MW;
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                                                                                                                                                                                                                                                                                                                                                                       53.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleoporin) (CAN protein).
                                                                                                                                                                                                               PROSITE; PS00038; HLH_1; 1. PROSITE; PS50888; HLH_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 PDAAPQCPAGS 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 PDAKTQCPDDS 11
                                    1MDY; 31-AUG-94
A29636; A29636.
S22587; S22587.
                                                                                                                                                                                                                                                                                                                                 318 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N214_HUMAN
P35658;
                                                          TRANSFAC;
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                                          PDB;
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MIM; 103390
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                      ö
        DISEASE: IN A CASE OF ACUTE UNDIFFERENTIATED LEUKEMIA (AUL) A HANNILOCATION RESULTS IN THE FORMATION OF A SET-CAN FUSION GENE. DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.; WWW-"http://www.infobiogen.fr/services/chromcancer/Genes/CAN.html".
                                                                                                                                                                                                 Pfam; PF03093; Nucleoporin_FG; 17.
SMART; SM00320; WD40; 1.
Nuclear protein; Transport; Proto-oncogene; Chromosomal translocation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shtivelman E., Cohen F.E., Bishop J.M.;
"A human gene (AHNAK) encoding an unusually large protein with a 1.2-
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neuroblast differentiation associated protein AHNAK (Desmoyokin)
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                                                                                                                                                                                                                                         11 X 5 AA APPROXIMATE REPEATS.
18 X 4 AA APPROXIMATE REPEATS.
11 X 3 AA APPROXIMATE REPEATS.
PRO/SER/THR-RICH.
LEUCINE-ZIPPER 1.
LEUCINE-ZIPPER 2.
                                                                                                                                                                                                                                                                                                                                Score 37; DB 1; Length 2090;
Pred. No. 2.5e+02;
L; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                              6DBE767FDD857F8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            microns polytonic rod structure. ";
Proc. Natl. Acad. Sci. U.S.A. 89:5472-5476(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 2960 AA.
                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                      BREAKPOINT
                                                                                                                                                                            Interpro; IPR004325; Nucleoporin_FG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Placenta;
MEDLINE=92302265; PubMed=1608957;
                                                                                                                                                                                                                                                                                                               213766 MW;
                                                                                                                                      EMBL; X64228; CAA45535.1; -.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                   53.68;
                                                                                                                                                 PIR; S26058; S26058.
Genew; HGNC:8064; NUP214.
MIM; 114350; --
                                                                                                                                                                                                                                                                                                                                                      6; Conservative
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998 DARTSCKDD 1006
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2085
2090
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is. In no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
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Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
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MEDILNE-97081760; PubMed-8923003;
Speck M., Barry F., Miller W.L.;
*Alternate promoters and alternate splicing of human tenascin-X,
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NW; F9FDD2103A35232A CRC64;
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Pred. No. 3.4e+02;
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MEDLINE-96015044; PubMed-8530023;
Tee M.K., Thomson A.A., Bristow J., Miller W.L.,;
"Sequences promoting the transcription of the human XA overlapping 9450c21A correctly predict the presence of adrenal-specific, truncated form of tenascin-X.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TENX_HUMAN STANDARD; PRT; 4289 AA. P22105; P78530; P78531; Q08424; Q9UMG7; O1-AUG-1991 (Rel. 19, Created) 16-QCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41; Last annotation update) Tenascin-X precursor (TN-X) (Hexabrachion-like).
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MEDLINE-93300909; PubMed-7686164;
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                                                                                                                                                             As Schalkwijk J., Zweers M.C., Steijlen P.M., Dean W.B., Taylor G.,
As Schalkwijk J., Zweers M.C., Steijlen P.M., Dean W.B., Taylor G.,
A van Vlijmen I.M., van Haren B., Miller W.L., Bristow J.;
The Arcessive form of the Ehlers-Danlos syndrome caused by tenascin-X deficiency.",
The Edition of the Ehlers-Danlos syndrome caused by tenascin-X and deficiency.",
The Engrish of the Ehlers-Danlos Syndrome caused by tenascin-X and Erwert and the Erwertlow. Appears To MEDIATE INTERACTIONS BETWEEN CELLS AND THE CELL MIGRATION. MAY PLAY A ROLE IN SUPPORTING THE GROWTH OF ENGRELIGIAR LOCATIONS. Extracellular matrix.

C. I. SUBGELIGIAR LOCATIONS. Extracellular and tissue fragility as observed in classical EDS, but lacking atrophic scars and delayed control in classical EDS, but lacking atrophic scars and delayed
                                      SEQUENCE OF 3470-4289 FROM N.A.
MEDLINE-89367293; PubMed-2475872;
Morel Y., Bristow J., Gitelman S.E., Miller W.L.;
"Transcript encoded on the opposite strand of the human steroid 21-hydroxylase/complement component C4 gene locus.";
Proc. Natl. Acad. Sci. U.S.A. 86:6582-6586(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS 19 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 32 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CAUTION: THERE ARE TWO GENES FOR TW-X: TRXA AND TWXB.
PARTIAL GENE WHICH CAN SOMETIMES RECOMBINE WITH THXB.
 other genes.";
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InterPro: IPR003961; FN_III.
InterPro: IPR003181; Flbrinogen_C.
InterPro: IPR002181; Flbrinogen_C.
InterPro: IPR002181; Flbrinom_EGF.
Pfam; PF00008; EGF; 15.
Pfam; PF000141; fals.
PRINTS; PR000147; flbrinogen_C; I.
PRINTS; SN00147; flbrinogen_C; I.
SNART; SN00181; EGF: 8.
SNART; SN00186; FBG; I.
SNART; SN00186; FBG; I.
gene with 5' and 3' ends buried in c
Hum. Mol. Genet. 5:1749-1758(1996).
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PS01186; EGF_2; 19
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PubMed=11642233;
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MIM; 606408;
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PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
Glycoprotein; Cell adhesion; Repeat; EGF-like domain; Colled
Extracellular matrix; Alternative splicing; Signal;
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EGF-LIKE 2.
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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US-09-824-647-4 69 1 PDAKTQCPDDST 12 Title: Perfect score: Sequence:

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671580 seqs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

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SPTREMBL_21:* Database:

sp_archea:* sp_bacteria:* sp_mammal:* sp_fungi:* sp_human;*

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sp_archeap:* sp_vertebrate: * sp_organelle:* sp_rodent:* sp_plant:* sp_virus:* sp_phage:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBL_TaxID=10095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhou J., Gao G., Crabb J.W., Serrero G.; "Purification of an autocrine growth factor homologous with mouse epithelin precursor from a highly tumorigenic cell line."; J. Blol. Chem. 268:10863-10869(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
PC cell-derived growth factor, PCDGF-EPITHELIN precursor homolog
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                       Length 589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 65; DB 11; Length 51;
Pred. No. 0.00012;
); Mismatches. 1; Indels
                                                                                                                                                Indels
                                                                PROSITE; PS00799; GRANULINS; 7.
PROSITE; PS00118; PA2_HIS; UNKNOWN_1.
SEQUENCE 589 AA; 63405 MW; 1DE8229C413CA292 CRC64;
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Last annotation update)
                                                                                                                   100.0%; Score 69; DB 11;
100.0%; Pred. No. 0.0003;
11ye 0; Mismatches 0;
                                                                                                                                                                                                                                                                    51 AA.
MGD; MGI:95832; Grn.
InterPro; IRR000118; Granulin.
InterPro; IPR001211; PhospholipaseA2.
Pfam; PF00396; granulin; 7.
SWART; SW00277; GRAN; 7.
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29 30
51 51
51 AA; 5473 MW;
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91.7%;
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                                                                                                                                                                                       PDAKTQCPDDST 219
                                                                                                             Query Match
Best Local Similarity 100.
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Best Local Similarity
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01-JUN-2002 (
01-JUN-2002 (
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01-MAY-2000
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CG13252.
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Q9QWB4
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                                                                             Length 384;
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Rhabdovíridae; Vesiculovírus.
                                                                                                                    Indels
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Rhabdoviridae; Vesiculovirus.
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY069266; AAL39411.1; -SEQUENCE 384 Aa; 42646 MW; 20AF3FIACA95954D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Virol. 64:4873-4883(1990).
EMBL; M35218; AAA48388.1; -
InterPro; IPR001903; Rhabd_glycop.
Pfam; PF00974; Rhabd_glycop.
SEQUENCE 511 AA; 57501 MW; 921EF8029D610957 CRC64;
                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TFEMBLrel. 17, Last annotation update)
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                                                                             Score 47;
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MEDLINE-90376442; PubMed-2168974;
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                                                                                                                                                                                                                                                                                                                                                                                                   (strain 83-HD-B2) glycoprotein.
                                                                             68.1%;
66.7%;
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Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                    Conservative
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Best Local Similarity
Matches 8; Conserv
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Length 511;

427 PDATSQLPDDET 438

Pred. No.

66.78;

089005

RESULT 6

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glycoprotein gene of vesicular stomatitis virus Indiana serotype
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MEDILINE-90376442; PubMed-2168974;
Bilsel P.A., Nichol S.T.;
"Polymerase etrors accumulating during natural evolution of the
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Pred. No. 5.6;
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Rhabdoviridae; Vesiculovirus.
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Rhabdoviridãe; Vesiculovirus.
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                                                  Created)
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66.7%;
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Best Local Similarity 66.7%;
Matches 8; Conservative
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EMBL; M35224; AAA48394.1; --
EMBL; M35221; AAA48391.1; --
EMBL; M35223; AAA48393.1; --
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Vesicular stomatitis virus
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427 PDATSQLPDDET 438
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Best Local Similarity
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01-NOV-1996
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Pred. No. 5.6;
1; Mismatches 3; Indels
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Vesicular stomatitis virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Rhabdoviridae; Vesiculovirus.
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                    Indels
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Rhabdoviridae; Vesiculovirus.
NCBL_TaxID=11276;
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InterPro; IPR001903; Rhabd_glycop.
Pfam; PF00974; Rhabd_glycop; 1.
SEQUENCE 511 AA; 5,7518 MW; 93B338029EB50177 CRC64;
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InterPro; IPR001903; Rhabd_glycop.
Pfam: PF00974; Rhabd_glycop; 1.
SEQUENCE 511 AA; 57484 MW; 687FB74FD58861F1 CRC64;
                                                                                                                                                                                                                                                        (TremBirel. 01, Last sequence update) (TremBirel. 17, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                  3;
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66.7%; Pred. No. 5.6;
iive 1; Mismatches 3
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                Mismatches
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                                                                                                                                                                                                                                                                                             (strain 86-GM-B) glycoprotein.
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66.78;
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Best Local Similarity 66.73
Matches 8; Conservative
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Best Local Similarity 66.7-
                                                                                             427 PDATSQLPDDET 438
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427 PDATSQLPDDET 438
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                  Conservative
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Best Local Similarity
Matches 8; Conserv
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RESULT 7 089008

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Gaps

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Indels

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Gaps
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                                                                                     Score 45; DB 12; Length 511;
Pred. No. 5.6;
1; Mismatches 3; Indels
InterPro; IPR001903; Rhabd_glycop.
Pfam; PF00974; Rhabd_glycop; 1.
SEQUENCE 511 AA; 57493 MW; 367C936F286E64E1 CRC64;
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089878

SO DE RESERVA DE LA COMPANSION DE LA COM

RESULT 10 Q89878

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Interpro; IPR000118; Granulin.
Pfam; PF00396; granulin; 3.
SMARE; SM00277; GRAN; 3.
PROSITE; PS00799; GRANULINS; UNKNOWN_2.
Alternative splicing; Hypothetical protein.
VARSPLIC 315. 358
AICCENTCCPAGYHOUSEDE
                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidee; Peloderinae; Caenorhabditis. MCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                            DQI -> FNFRPSAVRTLAAQPAITVLAVESARSTLKL
(IN ISOFORM T22H2.6B).
2AD5BBF9B70D1595 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                            -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; T22H2.6A (SHOWN HERE) AND T22H2.6B; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.9%; Score 42; DB 17; Length 463; 66.7%; Pred. No. 17; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                              Lennard N.; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00105; C5METTRFRASE.
TIGRRAMs; TIGR00675; dcm; 1.
PROSITE; PS00094; C5_MTASE_1; 1.
Methyltransferase; Complete proteome.
SEQUENCE 463 AA; 52202 MW; E63FF2F59A2IB18C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
NCBL_raxID=13773;
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 39.8 kDa protein T22H2.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
EMBL: AE009917; AAL64748.1; -
InterPro; IPR001525; C5_DNA_meth.
Pfam: PF00145; DNA_methylase; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 5;
Pred. No. 8.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      463 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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PubMed-11792869;
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Best Local Similarity 63.6
Matches 7; Conservative
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                                                                            Caenorhabditis elegans.
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Matches 8: Concern
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Seo H.C., Kube M., Edvardsen R.B., Jensen M.F., Beck A., Spriet E.,
Gorsky G., Thompson E.M., Lehrach H., Reinhardt R., Chourrout D.;
"The marine chordate Oikopleura dioica has a miniature genome.";
Science 0:0-0(2001).
                                                                                                                                                                                                                                                                                                                        "Polymerase errors accumulating during natural evolution of the glycoprotein gene of vesicular stomatitis virus indiana serotype isolates.";
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Olkopleuridae; Olkopleura.
NCBI_TaxID=34765;
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Rhabdoviridae; Vesiculovirus.
NCBI_TaxID=11276;
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                                                            511 AA.
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0; Mismatches
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090362; 090361;
01-MAY-2000 (TIEMBLIE]. 13, Created)
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                                                            PRT;
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Bilsel P.A., Nichol S.T.;
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70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                          Vesicular stomatitis virus.
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| 427 PDATSQLPDDET 438
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Best Local Similarity 70.0
Matches 7; Conservative
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Matches 8; Conservative
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                                                          PRELIMINARY;
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Query Match

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RESULT 11

Q8WPK9

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Gaps

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SEQUENCE

RESULT 12 Q9U362

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MEDINE-20020109; PubMed-11756688;
MEDINE-20020109; PubMed-11756688;
DelVecchio v.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T., Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N., Overbeek R.;
"The genome sequence of the facultative intracellular pathogen Brucella melitensis.";
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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                                                                                                                                               Brucella melitensis.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
NCBL_TaxID=29459;
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Pred. No. 7.9;
2; Mismatches 2; Indels
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Pred. No. 19;
2; Mismatches 3; Indels
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"Zebrafish granulin 1, 2, and hybrid cDNA sequences.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ARZ73479; AAK58708.1; -.
INTERPO: IRR000118; Granulin.
InterPro; IPR000221; WAP.
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PROSITE; PS00317; 4_DISULFIDE_CORE; UNKNOWN_1.
SEQUENCE 147 Aa; 16157 MW; 7A5D6864073A6CCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            506 AA; 55159 MW; C2F386ADBE79A999 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                01-MAR-2002 (TIEMBLrel. 20, Created)
1-MAR-2002 (TIEMBLrel. 20, Last sequence update)
01-JUN-2002 (TIEMBLrel. 21, Last annotation update)
Periplasmic dipeptide transport protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002)
EMBL, AAE096666, AAL5325.1, .
InterPro. IPR000914; SBP_bac_5.
Pfam; PF00496; SBP_bac_5; 1.
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                                   506 AA
                                   PRT;
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Best Local Similarity 58.3%;
Matches 7; Conservative
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Best Local Similarity 63.6%;
Matches 7; Conservative
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143 PIASTECPDPAT 154
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                                   PRELIMINARY;
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SEQUENCE 506 AA
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Q902D0
RESULT 14
Q8YD93
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2 DAKTQCPDDST 12

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39 DAQTVCPDGTT 49

Search completed: July Job time: 27.8462 secs

8, 2003, 16:27:58

Human ORF3242 prof

Human SAP-3 mature Human beta-defensi

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Scoring table:

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Human SAP-3 pre-pr Human beta-defensi Transplant media a Transplant media a Human beta-defensi Alpha-catenin 10.3 Human transcriptio

Orosophila melanog

glutamicum prote

Human ORFX protein Arabidopsis thalla

Propionibacterium

Composition containing antagonist of growth factor GP88 - useful for treating cancer and viral diseases and also for diagnosing disease

WPI; 1999-045276/04.

(SERR/) SERRERO G.

Serrero G;

Mouse granulin/epi Rat epithelin prec Human protein sequ Human epithelin pr Human cancer assoc Human GP88 autocri Granulin sequence.

AAE20520 AAR14325 AAB94550

AAW85474

100.0 100.0 89.0

Score

Result . 2 AAR14326 AAB43971 AAW85481 AAR48673

Propionibacterium Human polypeptide

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Propionibacterium
Propionibacterium
Mouse neuro-growth
Murine protein iso
Mouse TANGO 125 (T
Mouse neuro-growth
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AAO17781
AAO17766
AAU09708
AAB10600
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AA009709
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970S-0863079.
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antibody.
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Mouse GP88 autocri
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                                                                                               8, 2003, 16:08:55 ; Search time 35 Seconds (without alignments) 53.300 Million cell updates/sec
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| SIDS2/gcddata/geneseq_geneseq_embl./AA1986_DAT:*
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/SIDS2/gcgdata/genesegy/genesegp-emb1/AA2001.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:
                                                                                                                                                                                                                                                                                           908470
              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                      Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                             908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW85479
                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                          A_Geneseq_101002:*
                                                                                                                                                                                     1 SARGTKCLRKKIPR 14
                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                     US-09-824-647-5
73
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14
5889
5889
5889
589
621
621
593
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Database :

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ET-1 is a bifunctional growth regulator, capable of stimulating the growth of some cell types while inhibiting the growth of others. ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory bioactivity. "In contrast, however. ET-2 is apparently not capable of eliciting the growth stimulatory activity characteristic of ET-1 and, in fact, antegonises this ET-1 activity characteristic of ET-1 and, see also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GP88; granulin; epithilin; mouse; growth factor; autocrine; tumour; cancer; viral infection; antagonist; therapy; diagnosis.
                                                                                                                                                                                                   New cysteine-rich growth modulating proteins, epithelins - useful as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         344.362
/note= "K19T peptide, used to raise antibody"
562.575
/note= "S14R peptide, used to raise antibody"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208..219
/note= "P12T peptide used to raise antibody"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 73; DB 12;
100.0%; Pred. No. 9.8e-05;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "encoded by AGC" Misc-difference 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note- "encoded by TGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note- "encoded by CTG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse GP88 autocrine growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW85474 standard; Protein; 589 AA.
                                                                                                                                                                                                                                                                               Disclosure; Fig 23; 97pp; English.
                                    900S-0504508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    970S-0991862.
970S-0863079.
                                                                         (BRIM ) BRISTOL-MYERS SQUIB.
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                   910S-0083796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SARGTECLERKIPE 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SARGTKCLRKKIPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 14; Conservative
                                                                                                        Shoyab M, ' Plowman GD;
                                                                                                                                               WPI; 1991-325168/44.
N-PSDB; AAQ14340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       589 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-DEC-1997;
23-MAY-1997;
                                    03-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW85474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
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                                                                     This is the amino acid sequence of peptide S14R, comprising amino acid residues S56.R575 of murine GPB8 (see AAM85474). GF88 is an kDa glycoprotein autocrine growth factor that is expressed in a tightly regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which acts as a stringently required growth stimulator for the tumorigenic cells. S14R was used to raise neutralising antibodies to GP88. Antagonists to GP88, such as anti-GP88 antibodies, are used to treat diseases associated with increased expression of
                                                                                                                                                                                                                                          GP88, particularly cancer but also viral infections. Anti-GP88 antibodies can also be used as diagnostic reagents and to deliver toxins or other compounds to GP88-expressing cells.
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                                                                                                                                                                                                                                                                                                                                                      Length 14;
                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 73; DB 20;
100.0%; Pred. No. 2.4e-06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ET; growth regulation; inhibition; stimulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           280..335
/label- EP-1
/note- "claim 22, page 55"
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/label- EP-2
/note- "claim 23, page 55"
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/note= "claim 24, page 55"
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/note= "claim 25, page 55"
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/note= "claim 21, page 55"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= EP
/note= "claim 27, page 56"
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/note= "claim 28, page 56"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label- EP
/note- "claim 26, page 56"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR14327 standard; Protein; 589 AA.
                                    Example 8; Page 45; 86pp; English.
from altered GP88 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91WO-US02321
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SARGTKCLRKKIPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse epithelin precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .570
                                                                                                                                                                                                                                                                                                                                                                                           14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .416
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                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                    14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JAN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9115510-A:
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                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR14327;
                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
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                                                                                                                                                                                                                                                                                                                                                                                           Matches
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AAR14327
ID AAR
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Gaps

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Length 589; Indels us-09-824-647-5.rag

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15-JUN-2001; 2001US-0880842
                                                                                                                           WPI; 2002-267529/31.
                                                                                                                                                                                                                                                                                                                                                                                                                    589 AA;
                                                                             (SERR/) SERRERO G.
                                                                                                                                       N-PSDB; AAD32849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus rattus.
                                            3-MAY-1997;
                                                        08-DEC-1999;
28-FEB-2002
                                                                                                    Serrero G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR14325;
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                               protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
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                                                                                                                                                        This is the amino acid sequence of murine GP88, an 88 kDa glycoprotein autocrine growth factor and epithilin/granulin c precursor that is expressed in a tightly regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which acts as a stringently required c growth stimulator for the tumorigenic cells. Inhibition of GP88 c expression or action in the tumorigenic cells results in an inhibition of the tumorigenic properties of the overproducing cinhibition of the tumorigenic properties of the overproducing cells. Murine GP88 cDNA (see AAV82824) was obtained from the highly cumorigenic Ccell line. Antagonists to GP88 are used to treat diseases associated with increased expression of GP88, particularly cancer but also viral infections. Fragments of GP88 are used to reserve the authoridies (used as antagonists, as diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse, granulin precursor, GP88; cytostatic; tumourigenicity; tamoxifen; antineoplastic; antioestrogen therapy; skin cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                         Composition containing antagonist of growth factor GP88 - useful for treating cancer and viral diseases and also for diagnosing disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Regions used as antigens to raise anti-GP88 antibodies"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         562..575
/note= "Regions used as antigens to raise anti-GP88
                                                                                                                                                                                                                                                                                                                        expressing cells) and to screen for antibodies. Methods are provided for diagnosing disease, or determining susceptibility disease, resulting from altered GP88 activity.
                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                               reagents and for delivering toxins or other compounds to GP88-
                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 73; DB 20; Length 589; 100.0%; Pred. No. 9.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse granulin/epithelin precursor (GP88) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note- "Encoded by ACA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Unknown
/note= "Encoded by ATG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE20520 standard; Protein; 589 AA.
                                                                                                                                       Example 5; Fig 8A-D; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                from altered GP88 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibodies"
586
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SARGTKCLRKKIPR 14
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                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
nes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      344..362
                                                       WPI; 1999-045276/04.
                                                                                                                                                                                                                                                                                                                                                                       589 AA;
           (SERR/) SERRERO G.
                                                                   N-PSDB; AAV82824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-2002
                                  Serrero G;
                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE20520;
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
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The invention relates to a method for diagnosing tumourigenicity in a human. The method comprises obtaining a biological sample containing cells from the patient, detecting GPBB in the cells of the sample, and determining the number of GPBB positive cells in the sample, and determining the ratio of GPBB positive cells to the total number of cells in the sample. The invention also relates to a method for determining if a human patient is resistant to the antineoplastic effects of tumourigenicity in a sample, such as blood, serum, plasma, urine, nipple apprate, cerebrospinal fluid, liver, kidney, breast, bone, brain, lung, colon, or skin cancer. The method can be used to treat or prevent re-occurrence of cancer in a patient, by administering tamoxifen if the sample contains less than 10 % GPBB, or less than 5 % GPBB positive cells. The present sequence is mouse granulin/epithelin precursor (GPBB)
                                                                                                                                                                                                                                                                        comprising obtaining a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 73; DB 23;
100.0%; Pred. No. 9.8e-05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ET; growth regulation; inhibition; stimulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          page 54"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "claim 13, page 54"
59..114
/label= EP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           page 54
                                                                                                                                                                                                                                                                          Diagnosing tumorigenicity in a human, com sample, detecting GP88 in the cells, and positive cells in the sample -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR14325 standard; Protein; 589 AA.
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/label= EP-1
/note= "claim 12, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= precursor
/note= "claim 11,
                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 8; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label- EP-2
970S-0863079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 562 SARGTKCLRKKIPR 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SARGTKCLRKKIPR 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity luv...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205..261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat epithelin precursor.
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Peptide

Peptide

Peptide

Peptide

03-APR-1991;

17-0CT-1991. WO9115510-A.

13-MAR-1991; 03-APR-1990;

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polynucleotide which comprises a 3'-end sequence, where the coligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13631 to AAH18742 represent human cDNA sequences; AAB92446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invertion describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligoral primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer sets for synthesizing polynucleotides, particularly the 5602 full-length coluss defined in the specification, and for the detection and/or diagnosts of the abnormality of the proteins encoded by the full-length coluss
                                                                                                                                                                                                                                                                                                            Ota T, Isogal T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 58; DB 22; Length 413;
Pred. No. 0.035;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; SEQ ID 15310; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ET; growth regulation; inhibition; stimulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR14326 standard; Protein; 593 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUL-2000; 2000EP-0116126
                                                                                            99JP-0300253
2000JP-0118776
                                                                                                                                                                                         09-JUN-2000; 2000JP-0241899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SARGTKCLRKKIPR 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                           (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-318749/34.
                                                                                               27-AUG-1999;
11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JAN-1992
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                                                                                                                                                              02-MAY-2000;
                                                              29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ET-1 is a bifunctional growth regulator, capable of stimulating the growth of some cell types while inhibiting the growth of others. ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory bloactivity. In contrast, however, ET-2 is apparently not capable of ellciting the growth stimulatory activity characteristic of ET-1 and,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New cysteine-rich growth modulating proteins, epithelins - useful as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in fact, antagonises this ET-1 activity.
See also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 65; DB 12; Length 58
Pred. No. 0.0027;
1; Mismatches 1; Indels
                                                    /label- BP
/note- "claim 15, page 54"
   "claim 14, page 54"
                                                                                                                                                        /label- EP
/note- "claim 16, page 54"
                                                                                                                                                                                                                                                                                         54"
                                                                                                                                                                                                                                                                                                                                                    /label= EP
/note= "claim 18, page 55"
                                                                                                                                                                                                                                                    /label- EP
/note= "claim 17, page
515..570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB94550 standard; Protein; 413 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 18; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.0%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91WO-US02321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91US-0083796
90US-0504508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BRIM ) BRISTOL-MYERS SQUIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SARGTKCLRKKIPR 14
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Best Local Similarity 85.7
Matches 12; Conservative
                                                                                                                                .416
                                                                                                                                                                                                                      .495
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N-PSDB; AAQ14338.
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Gaps

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EP1074617-A2 Homo sapiens

26-JUN-2001

AAB94550;

AAB94550 RESULT

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Sequence

07-FEB-2001.

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antidiabetic; antiasthmatic; antimerary; immunous antidiabetic; antiasthmatic; antimerary; antidiabetic; antiasthmatic; antiallergic; antibacterial; antiviral; antidiabetic; antithyroid; antiallergic; antibacterial; antiviral; dermatological; neuroprofective; cardiant; thrombolyfic; coagulant; nootropic; antipsoriate and antianglogenic. The polynucleotides and polypeptides can be used for preventing, treating or meliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of manner cells, to treat disorders of haematopoletic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate

inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities
                                               diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antrheumatic; antiarthritic; antiviral; antidiammatory; antityroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; haematopoietic cell disorder; autoimmune disorder; haematopoietic call disorder; autoimmune disorder; haemostatic; cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer -
                            cancer associated gene; cancer antigen; detection; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lnclude: cytostatic; proliferative; vulnerary; immunomodulator;
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pred. No. 0.052;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 2094-2096; 2352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW85481 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
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Best Local Similarity 71.4
Watches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM;
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                                                                                                                                                                                                                                                                                                                                                                                                                               WO200055350-A1.
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-MAR-1999;
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   NAMES OF COLOR OF STREET STREE
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Pred. No. 0.05;
3; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "claim 8, page 55"
                                                                                           53
                                                                                                                                                                                 53
                                                                                                                                                                                                                                                                                                                                                                  page 53"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    534
                                                                                                                                                                                                                                                                          "claim 4, page 53"
note= "claim 1, page
                                                                                                                                                                                       page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 22; 97pp; English.
                                                                                                                                                                                 claim 3,
                                                                                                                                                                                                                                                                                                                                                                                                                               'label= EP
'note= "claim 6,
                                                                                                                                                                                                                                                                                                                                                                  "claim 5,
                                                                                        "claim 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note- "claim 7,
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|larity 71.4%;
|Conservative
                                                                                                                                                    label- EP-2
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                                                                                                                                                                                                                                             label- EP
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                            ..337
                                                                                                                                                                                       note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shoyab M, Plowman GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1991-325168/44.
N-PSDB; AAQ14339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             593 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAR-1991;
03-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9115510-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB43971;
                               Protein
                                                                                                                     Protein
                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                      Pept1de
                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB43971
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0; Gaps

EXEXEXE Exexexe

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AL.

16-DEC-1997; 23-MAY-1997; 22-MAY-1998; 26-NOV-1998

antibody.

GP88;

Serrero G;

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GP88; granulin; epithilin; human; growth factor; autocrine; tumour;
cancer; viral infection; antagonist; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The granulin inhibits keratinocytes and is useful in formulations for promoting the healing of wounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New cystine riph granulin peptide(s) from leucocyte(s) - are keratinocyte inhibitors useful topically for wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      340..364
/note= "E19V peptide used to raise antibody"
566..579
/note= "A14R peptide used to raise antibody"
                                                                 /note= "Glycine encoded by CAG."
/note= "Valine encoded by ATG."
539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 53; DB 14
Pred. No. 0.4;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Figure 4c; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW85475 standard; Protein; 593 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human GP88 autocrine growth factor.
                                                                                                                                                                                                      92WO-CA00089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 72.6%;
Best Local Similarity 75.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-US10555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0991862.
97US-0863079.
                                                                                                                                                                                                                                                      92US-0829233.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      568 RGTKCLRREAPR 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 RGTKCLRKKIPR 14
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1993-320328/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-045276/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ი
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            593 AA;
                                                                                                                                                                                                                                                                                                    (SOLO/) SOLOMON S.
                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAQ49052
                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SERR/) SERRERO
                                                                                                                                                                                                                                                      3-FEB-1992a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9852607-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-DEC-1997;
23-MAY-1997;
                                                                                                                                                                                                      28-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-NOV-1998
                                                                                                               W09315195-A.
                                                                                                                                                             05-AUG-1993
                                                                                                                                                                                                                                                                                                                                                  Solomon S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Serrero G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW85475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
AAW85475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the amino acid sequence of peptide A14R, comprising amino acid residues A566-R579 of human GP08 (see AAM05475). GP08 is an 88 kba glycoprotein autocrine growth factor that is expressed in a tightly regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which acts as a stringently required growth stimulator for the tumorigenic cells. A14R was used in an attempt to raise neutralising antibodies to GP08 (see also AAW03480). Antagonists to GP08, such as anti-GP08 antibodies, are used to treat diseases associated with increased expression of GP08, particularly cancer but also viral infections. Anti-GP08 antibodies can also be used a diagnostic reagents and to deliver toxins or other compounds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Composition containing antagonist of growth factor GP88 - useful for treating cancer and viral diseases and also for diagnosing disease from altered GP88 expression
                                                                                                               granulin; epithilin; human; growth factor; autocrine; tumour; r; viral infection; antagonist; therapy; diagnosis; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Granulin; keratinocytes; wound healing; inhibition; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 14;
                                                                 Human GP88 autocrine growth factor antigenic peptide A14R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 53; DB 20;
Pred. No. 0.0098;
2; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key Location/Qualifiers
Misc-difference 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR48673 standard; Protein; 593 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 8; Page 45; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.6%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                  98WO-US10555.
                                                                                                                                                                                                                                                                                                                                                                                              97US-0991862,
97US-0863079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 75.u.,
Best Local Similarity 75.u.,
                     15-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  granulocytes; leucocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 RGTKCLRKKIPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GP88-expressing cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-045276/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Granulin sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SERR/) SERRERO G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 AA;
                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                      WO9852607-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-APR-1994
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AAR48673;

RESULT 10 AAR4867

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Sequence

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Gaps

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Length 593; Indels

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WPI; 2002-106200/14
                                                                                                                                                                                                                                              593 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                             08-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leach MD,
                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         ABP34269;
                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                          protein.
                                                                                                                                                                                                                                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                                                            ABP34269
                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; granulin precursor; GP88; cytostatic; tumourigenicity; tamoxifen; antineoplastic; antioestrogen therapy; skin cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Region used as antigen to develop anti-human
                                                                                                                                                                                                                                                                                                              Gaps
                     Composition containing antagonist of growth factor GP88 - useful for treating cancer and viral diseases and also for diagnosing disease from altered GP88 expression
                                                                                                                         derived from normal cells, and which acts as a stringently required growth stimulator for the tumorigenic cells. Inhibition of GP88 expression or action in the tumorigenic cells. Inhibition of the tumorigenic cells. Inhibition of the tumorigenic cells results in an inhibition of the tumorigenic properties of the overproducing cells. Antagonists to GP88 are used to treat diseases associated with increased expression of GP88 particularly cancer but also viral infections. Fragments of GP88 are used to raise specific antibodies (used as antagonists, as diagnostic reagents and for delivering toxins or other compounds to GP88 expressing cells) and to screen for antibodies. Methods are provided for diagnosing disease, or determining susceptibility to disease, resulting from
                                                                                              glycoprotein autocrine growth factor and epithilin/granulin precursor that is expressed in a tightly regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells
                                                                                                                                                                                                                                                                                        DB 20; Length 593;
                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                   an 88 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human granulin/epithelin precursor (GP88) protein.
                                                                                    This is the amino acid sequence of human GP88,
                                                                                                                                                                                                                                                                                        Score 53; DB 2
Pred. No. 0.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GP88 neutralising antibody
                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Encoded by AAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         AAE20521 standard; Protein; 593 AA.
                                                               Example 5; Fig 9A; 86pp; English.
                                                                                                                                                                                                                                                                                        72.6%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2001; 2001US-0880842.
                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                             568 RGTKCLRREAPR 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346..364
                                                                                                                                                                                                                                                                                                                                  3 RGTKCLRKKIPR 14
                                                                                                                                                                                                                                              altered GP88 activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-267529/31.
N-PSDB; AAD32850.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SERR/) SERRERO G.
                                                                                                                                                                                                                                                                   593 AA;
N-PSDB; AAV82825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2002025543-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAY-1997; 08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serrero G;
                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              AAE20521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                      cells
                                                                                                                                                                                                                                                                                        human. The method comprises obtaining a biological sample containing cells from the patient, detecting GP88 in the cells of the sample, and determining the number of GP88 positive cells in the sample, and determining the number of GP88 positive cells in the sample, and determining the ratio of GP88 positive cells to the total number of cells in the sample. The invention also relates to a method for determining if a human patient is resistant to the antineoplastic effects of antioestrogen therapy. The method is useful for diagnosing unmourigenicity in a sample, such as blood, serum, plasma, urine, nipple aspirate, cerebrospinal fluid, liver, kidney, breast, bone, brain, lung, colon, or skin cancer. The method can be used to treat or prevent re-occurrence of cancer in a patient, by administaring tamoxifen if the sample contains less than 10 % GP88, or less than 5 % GP88 positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; diamune modulation; hamantopolesis regulation; tissue growth; anglogenesis; activin; inhibit; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; vasotropic; antipsorlatt; antidiabetic; cytostatic; noctropic; eardiatherosclerotic; anticoaquiant; thrombolytic; cardiatherosclerotic; antinflammatory; immunomodulator;
Diagnosing tumorigenicity in a human, comprising obtaining a cell sample, detecting GPB8 in the cells, and determining the number of GPB8 positive cells in the sample -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                             The invention relates to a method for diagnosing tumourigentialty in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiant; hypotensive; antithyroid; antiinflammatory; immunom
dermatological; analgesic; virucide; antibacterial; fungicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 23; Length 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.6%; Score 53; DB 2
75.0%; Pred. No. 0.4;
11ve 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ORF3242 protein, SEQ ID NO:6484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP34269 standard; Protein; 51 AA.
                                                                                                                                                                                 Disclosure; Fig 9B; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-MAY-2001; 2001WO-US17076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-MAY-2000; 2000US-206690P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1111111:: 11
568 RGTKCLRREAPR 579
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Matches 9; Conservative
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Wang SS, Bhatia A;

Carter D;

Mitcham Jī, , Jen S, Ça

Persing DH,

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Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID No 8311; 1069pp; English
                                                                                       21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                      20-APR-2001; 2001WO-US12865
                                                                                                                                                                                                                      L'maisonneuve J, Zhang Y,
                                                                                                                                                                                                                                                        WPI; 2001-616774/71.
                                                                                                                                                                (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                           N-PSDB; AAS59537
                      01-NOV-2001
                                                                                                                                                                                                    Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU41864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences ABP31028-ABP35561 represent 4534 novel human proteins designated OFF (open reading frame) 1-4534, and sequences ABN75054-ABN79587 represent cDNAs encoding them. The invention also encompasses polypeptides at least 80% identical to the ORF1-ORF4534 (collectively referred to as ORFX) proteins, polynucleotides at least 85% identical to the ORF2 nucleotides. The recombinant production of ORFX proteins at neithodies specific for ORFX proteins, methods of detecting ORFX proteins, antibodies specific for ORFX proteins, methods of detecting ORFX proteins and propaptides, methods of screening for modulators of ORFX expression or activity, and methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide range of biological activities, such as cytokine, cell proliferation, cell differentiation, immune modulation, haematopolesis regulation, tissue growth, anglogenesis, activity, thrombolytic activity, chemotactic/chemokinetic activity, haemostatic activity, thrombolytic activity, receptor/ligand, antiliflammatory activity, thrombolytic activity, receptor/ligand, antiliflammatory activity, thrombolytic activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurological disorders such as epilepsy and Alzheimer's disease, cardiovascular diseases, immune system disorders, disorders related to organ transplantation, disorders of tissue growth and regeneration, diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester stronge disease, and infectious diseases caused by viral, bacterial, fungal and other pathogens. OFFX nucleic acids may also be used as a source of primers and probes, in the detection of OFFX genomic sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                      and antiinfective activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. OREX proteins, nucleic acids and antibodies may be used in the treatment of cancers, other proliferative disorders such as psoriasis and benign tumours,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or transcripts, in the identification and cloning of homologous sequences, in genetic diagnosis, and in forensic biology. The ORFX nucleic acids may additionally be used to produce transgenic animals which may be useful for studying the function and/or activity of ORFY protein, and in drug screening. The ORFX proteins may also be used as immunogens to generate specific antibodies, which are useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                 Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis, treatment and monitoring of ORFX-associated diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB 23; Length 51;
Pred. No. 2.2;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes immunogenic protein #8012.
                                                                                                                       Claim 10; Page 1869; 2508pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU47116 standard; Protein; 76 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.9%;
80.0%;
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Best Local Similarity 80.uv,
Best Local Similarity 80.uv,
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GTKCLHLKIP 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 AA;
N-PSDB; ABN78295.
                                                                                         transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200181581-A2.
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                                                        preventing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38
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                                     Novel
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the infilammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enzyme linked immunosorbent assay (ELISA).
Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA)
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12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
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Pred. No. 12;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity 50...
6; Conservative
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RGRRCRRRSLPR 12
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us-09-824-647-5.rag

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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAHRO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgarie. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).
                                                                                                                                                                                                                                                                                                                                                                   Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                          ", Wang SS, Bhatla A;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; SEQ ID No 3059; 1069pp; English.
                                                                                                                                                                                                                                          Mitcham JL,
                                                                                                                                                                                                                                                              Jen S,
                                                            20-APR-2001; 2001WO-US12865.
                                                                                                   21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                            L'maisonneuve J, Zhang Y,
                                                                                                                                                                                                                                       Persing DH,
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N-PSDB; AAS59515.
                                                                                                                                                                                             (CORI-) CORIXA CORP
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                    01-NOV-2001
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XEX#X###X####X####X####X######
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Query Match 54.8%; Score 40; DB 22; Length 85; Best Local Similarity 53.8%; Pred. No. 13; Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps

2 ARGTKCLRRKIPR 14 ||| ||| :: | 57 ARGVLCLRSRVAR 69

2 4

Search completed: July 8, 2003, 16:24:15 Job time: 36 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 8, 2003, 16:21:00; Search time 8.61539 Seconds (without alignments) 47.812 Million cell updates/sec Run on:

US-09-824-647-5 73 1 SARGTKCLRKKIPR 14

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

262574 seqs, 29422922 residues Searched:

262574 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:* Database :

/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* /cgn2_6/ptodata/1/iaa/backfiles1.pep:* /cgn2_6/ptodata/1/1aa/6B_COMB.pep: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.p /cgn2_6/ptodata/1/laa/5A_COMB.pep: /cgn2_6/ptodata/1/laa/5B_COMB.pep: /cgn2_6/ptodata/1/laa/6A_COMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

	Appli	Appli	Appli	Appli	Appli	Appli	App11	App1i	Appli	Appli	App1:	App11	Appli	Appli	Appli	, Appl		Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli
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Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
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h DB ID	4	9 1 US-07-668-648-6	~	9 2 US-08-431-333-6	4	S	-	7	9 2 US-08-431-333-2	9 5 PCT-US91-02321-2	3 1 US-07-668-648-4	3 2 US-08-429-998-4	3 2 US-08-431-333-4	3 5 PCT-US91-02321-4	4	3 4 US-08-991-862-17	4	_ س	3	4	3 4 US-09-566-906-5	-	1 1 US-08-003-311B-2	1 1 US-08-261-432-2	ß	4	8 2 US-08-937-540-2
Query Match Length DB	14	589	583	589	589	589	589	589	583	589	593	593	593	593	14	59	278	263	263	263	263	821	821	821	821	520	298
Query	100.0	100.0	100.0	100.0	100.0	100.0	89.0	89.0	89.0	89.0	79.5	79.5	79.5	79.5	72.6	72.6	54.8	52.1	52.1	52.1	52.1	52.1	52.1	52.1	52.1	49.3	49.3
Score	73	73	73	73	73	73	65	65	65	65	58	58	28	58	53	53	40	38	38	38	38	38.	38	38	38	36	36
Result No.	1	7	Э	7	S	9	7	80	6	10	11	12	13	14.	. 15	16	17	18	19	20	21	22	23	24	25	56	27

26, Appl	7, Appli	7, Appli	7, Appli	7, Appli	7, Appli	7, Appli	16, Appl	22, Appl	2, Appli	6, Appli	6, Appl1	6, Appli	6, Appli	71, Appl	72, Appl	Ċ	25, Appl	
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	
1-26	:-2	1-7	1-7	.7	-7	.7	.16	-22	ç	. ب	.و	9-1	9-1	1-71	1-72	3-17	-25	
JS-09-398-395A-26	JS-08-112-208C-	IS-08-248-819A-	JS-08-337-646A-	IS-08-856-531-	JS-08-856-034-7	-08-927-326	JS-09-309-487-	JS-09-309-487-2	-09-230-421	JS-08-589-446-6	-08-444-883·	JS-08-389-459A-6	-08-987-867	JS-08-679-493A-	JS-08-679-493A-	IS-08-468-847B-	JS-09-253-316-2	
as	ns	ΩS	ns	as	OS	ns	as	a	ΩS	as	ΩS	ns	ns	as	a	OS	ΩS	
4	Н	Н	~	7	7	4	4	4	4	Н	Н	~	m	4	4	Н	7	
598	41	41	41	41	41	41	9/	92	301	314	314	314	314	327	327	357	357	
49.3	47.9	47.9	47.9	47.9	47.9	47.9	46.6	46.6	46.6	46.6	46.6	46.6	. 46.6	46.6	46.6	46.6	46.6	
36	35	35	32	35	35	35	34	34	34	34	34	34	34	34	34	34	34	
28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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Gaps
                             GENERAL INFORMATION:
APPLICANT: Serrero, Ginette
APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REPERENCE: 2996.488/P001-A
CURRENT APPLICATION NUMBER: US/08/991,862
CURRENT FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/863,862
EARLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                        , LACATION: (1)...(14)
; OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the corner information: antisera against the GP88 used in the GPHER INFORMATION: Immunoaffinity step.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 73; DB 4; Length 14; 100.0%; Pred. No. 2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
Sequence 5, Application US/08991862 Patent No. 6309826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/07668648 Patent No. 5416192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SARGTKCLRKKIPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SARGTKCLRKKIPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Conservative
                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: mouse granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS-07-668-648-6
                                                                                                                                                                                                                                                               SEQ ID NO 5
LENGTH: 14
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Aguert No. 541619.
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
APPLICANT: Plowman, EFFTHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVERTION: PPTTHELING PROTEINS 1: Pennie & Edmonds 1155 Avenue of the Americas APPLICANT: Plowman, Greg TITLE OF INVENTION: BPIT TITLE OF INVENTION: MOD NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: ADDRESSE: Pennie & Ed STREET:

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Sequence 2, Application US/08991862; Patent No. 6309826; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             562 SARGTKCLRKKIPR 575
                                                                                                                                                                                                                                          : 589 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (212) 869-9741 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 589 amino acids
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                                                                                                                                                                                                                    1 SARGTKCLRKKIPR 14
                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-431-333-6
                      ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-429-998-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
GX: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                           RESULT 4
US-08-431-333-6
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  LENGTH:
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APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROFEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 589
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    COUNTRIE ....

2. COUNTRIE ....
2. LP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,648
FILING DATE: 19910819
CLASSIFICATION: 514
ATGORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,998
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 73; DB Best Local Similarity 100.0%; Pred. No. 6.1 Matches 14; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMDTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08429998
Patent No. 5885961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELECOMMUNICATION INFORMATION
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    : 589 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-668-648-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U
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  COUNTRY:
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STATE:
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Gaps
DB 2; Length 589;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,333
ELLING DATE: 27-APR-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 73; DB 2; I
Best Local Similarity 100.0%; Pred. No. 6.1e-05;
Matches 14; Conservative 0; Mismatches 0;
                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REPERENCE_POCKET NUMBER: 5624-161-999
TELECOMENICATION INFORMATION:
TELEPHONE: (212)790-9090
                                                                                                                                                                                                                                                       Sequence 6, Application US/08431333
Patent No. 5965723
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: MODULATING PROTEINS:
100.0%; Score 73; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COUNTRY:
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APPLICANT: Serrero, Ginette
1TILE OE INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996-188, P001-A
CURRENT APPLICATION NUMBER: US/08/991,862
CURRENT FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/863,862
EARLIER APPLICATION NUMBER: 09/05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VAI: 2.0
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GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 589;
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                                                                                                                                                                                                                                                                                                          6.1e-05;
                                                                                                                                                                                                                                                                                        DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: EPITHELINS: NOVEL CYST
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company
STREET: 3005 First Avenue
                                                                                                                                                                                                                                                                                      100.0%; Score 73; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: 0N0071A-PC
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US91/02321
FILING DATE: 19910403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                             ORGANISM: Mouse epithelin/granulin US-08-991-862-2
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                                                                                                                                                                                                                                                                                                                                                               : 589 amino acids
AMINO ACID
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                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 14; Conservative
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Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98121
                                                                                                                                                        SEQ ID NO 2
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                                                                                                                                                                                                               TYPE: PRT
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Gaps
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                                                   APPLICANT: Shoyab, Monamuscu APPLICANT: Shoyab, Monamuscu APPLICANT: Plowman, Gregory D. TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH TITLE OF INVENTION: MODULATING PROFEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOVEL CYSTEINE-RICH GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 589;
                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/668,648 FILING DATE: 19910819
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Pred. No. 0.0014;
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                                                                                                                                       STREEF: 1155 Avenue of the Americas CITY: New York COUNTRY: USA XTD: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSEE: Pennie & Edmonds
F: 1155 Avenue of the Americas
New York
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-429-998-2; Sequence 2, Application US/08429998; Patent No. 5885961
Sequence 2, Application US/07668648 Patent No. 5416192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18,872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 89.0%;
Best Local Similarity 85.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 589 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SARGTKCLRKKIPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (212) 869-9741
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-07-668-648-2
                                                                                              TITLE OF INVENTION: EP.
TITLE OF INVENTION: MOI
NUMBER OF SEQUENCES: 1.
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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OPERATING SYSTEM:
                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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Gaps

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Length 589;

Score 65; DB 2; Pred. No. 0.0014;

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Sequence 4, Application US/O7668648

Patent No. 5416192

GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
                                                                                                                                                                                                                                                    Sequence 2, Application PC/TUS9102321
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE, ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPALILLO
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02321
PTING DATE: 19910403
                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Bristol-Myers Squibb Company
STREET: 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: POOY, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/POCKET NUMBER: 0000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.0%;
                                                                                                                             : 589 amino acids
AMINO ACID
                                                                                                       1 SARGTKCLRKKIPR 14
                                                              Conservative .
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 12; Conserv
                                      Local Similarity
es 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Seattle
STATE: Washingt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                    PCT-US91-02321-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-07-668-648-4
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                      Query Match
                                                                                                                                                                                                                RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08431333
Fatent No. 5965723
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D:
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROFIEINS
CORRESPONDENCES: 12
CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
CORRESPONDENCES: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITT: New York
COUNTRY: UGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,333
FILING DATE: 27-APR-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 65; DB 2;
Pred. No. 0.0014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 5624-161-999
ELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
                                                                                                                                             NAME: Misrock, S. Leslie
REGISTRATION UNDBER: 18.872
REFERENCE/DOCKET NUMBER: 5624-161-999
RELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872,161.0
                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
US/08/429,998
                                                                                                                                                                                                                                  TELEPHONE: (212)790-9090
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 589 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                          : 589 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SARGTKCLRKKIPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 89.03
Best Local Similarity 85.73
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                         ; TOPOLGY: linear;
; MOLECULE TYPE: protein
US-08-429-998-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-431-333-2
APPLICATION NUMBER:
                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 10036
                                                                                                                                                                                                                                                                                                                       LENGTH:
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DB 5; Length 589;

Score 65; Pred. No.

Gaps

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Length 593;發
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Pred. No. 0.023;
                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,333
FILING DATE: 27-APR-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                 Score 58; DB 3
Pred. No. 0.023
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08431333
Patent No. 5965723
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CONTINUED OF INVENTION: MODULATING PROFEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 4, Application PC/TUS9102321
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 54
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.5%;
71.4%;
                                                                                                                               Query Match 79.5%;
Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   566 AARGIKCLRREAPR 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 593 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212) 869-9741 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                 1 SARGTKCLRKKIPR 14
SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Conservative
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                                                                 MOLECULE TYPE: protein US-08-429-998-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Plowman, TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 10; Conserve
                                      amino acid
                                                         linear
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New York
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                                                       FOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-431-333-4
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Patent No. 5885961
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,648
FILING DATE: 19910819
CLASSIFCATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MASIOCK, S. Leslie
REGISTRATION NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFANCE, (212) 869-9741
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/08/429,998
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 58;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MISTOCK, S. Leslie.
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 56
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.5%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 869-9741 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SARGTKCLRKKIPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 593 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-668-648-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 10; Conserva
                                                                                                                OPERATING SYSTEM:
  New York
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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Gaps
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TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/08/991,862
CURRENT FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/863,862
EARLIER FILING DATE: 1997-05-23
NUMBER OF SEO ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : LOCATION: (1)..(14)
: OTHER INFORMATION: Internal peptide of human GP88 used to develop
: OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
US-08-991-862-7
                                             EPITHELINS: NOVEL CYSTEINE-RICH GROWTH MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5; Length 593; 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.6%; Score 53; DB 4; Length 14; 75.0%; Pred. No. 0.0055; 1ve 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                      SOUTHWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02321
FILING DATE: 19910403
CLASSIFICATION: 514
                                                                                                                         E: Bristol-Myers Squibb Company 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.5%; Score 58; 71.4%; Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: POOR, Brian W.
REGISTRATION NUMBER: 32,928
REPERENCE/DOCKET UNMBER: ON0071A-PC
TELECOMMUNICATION:
TELEPHONE: (206)728-4800
                                                                                                                                                                                                                                                            OMFUTER READABLE FORM:
BEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08991862
Patent No. 6309826
    Shoyab, Mohammed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :1111111:: 11
566 AARGTKCLRREAPR 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SARGTKCLRKKIPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 79.5
Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 72.6
Best Local Similarity 75.0
Matches 9; Conservative
                    APPLICANT: Plowman, GreatITLE OF INVENTION: EPITILE OF INVENTION: MODINER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein
PCT-US91-02321-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Human granulin
                                                                                                                                                               CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: PEPTIDE
                                                                                                                              ADDRESSEE:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-08-991-862-7
                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 7
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Gaps

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3 RGTKCLRKKIPR 14
                  3 RGTKCLRREAPR 14
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Search completed: July 8, 2003, 16:30:19 Job time: 9.61539 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein

July 8, 2003, 16:24:26; Search time 13.641 Seconds Run on:

(without alignments) 119.483 Million cell updates/sec

US-09-824-647-5 73 Title: Perfect score:

1 SARGTKCLRKKIPR 14 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

445758 seqs, 116419773 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_RUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:* 'cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep: '
'cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep: '
'cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep: ' 'ptodata/2/pubpaa/US08_NEW_PUB.pep:'
'ptodata/2/pubpaa/US08_PUBCOMB.pep:'
'ptodata/2/pubpaa/US09_NEW_PUB.pep:'
'ptodata/2/pubpaa/US09_NEW_PUB.pep:' /pubpaa/US06_NEW_PUB.pep otodata/2/pubpaa/US07_ Published_Applications_AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 5, Appli		Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	'n	Sequence 1416, Ap	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli	7	7		Sequence 17, Appl
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a	US-09-824-647-5	US-10-218-509-5	US-10-281-160-5	US-09-813-156-5	US-09-824-807-5	US-09-824-647-2	US-10-218-509-2	US-10-281-160-2	US-09-813-156-2	US-09-824-807-2	US-09-925-301-1416	US-09-824-647-7	.US-10-218-509-7	US-10-281-160-7	US-09-813-156-7	US-09-824-807-7	US-09-824-647-17	US-10-218-509-17	US-10-281-160-17
BG	6	σ	σ	10	10	σ	σ	6	10	2	2	σ	0	9	ដ	10	6	6	6
% Query Match Length DB	14	14	14	14	14	589	589	589	589	583	621	14	14	14	14	14	593	593	593
& Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	79.5	72.6	72.6	72.6	72:6	72.6	72.6	72.6	72.6
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Sequence 17, Appl Sequence 692, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 570, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 26, Appl Sequence 7, Appli Sequence 26, Appl Sequence 26, Appl Sequence 26, Appl Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 3, Appli Sequence 3, Appli Sequence 27, Appli Sequence 3, Appli Sequence 27, Appli
10 US-09-813-156-17 10 US-09-824-807-17 9 US-09-866-050A-692 9 US-09-780-264-15 10 US-09-790-264-15 10 US-09-872-822-3 10 US-09-917-340-72 10 US-09-917-340-72 10 US-09-917-340-72 10 US-09-917-340-52 9 US-09-917-340-52 9 US-09-917-340-72 10 US-09-917-340-72 10 US-09-917-340-72 10 US-09-17-85-2 10 US-09-764-853-697 10 US-09-764-853-697 10 US-09-900-797-26 10 US-09-900-797-26 10 US-09-900-797-26 10 US-09-900-797-26 10 US-09-887-586A-26 10 US-09-900-797-26 10 US-09-900-797-26 10 US-09-887-586A-26 10 US-09-900-797-26 10 US-09-900-797-26 10 US-09-900-797-26 10 US-09-900-797-26 10 US-09-900-797-26 10 US-09-900-797-26 10 US-09-900-797-26
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ALIGNMENTS

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Gaps
                                                                          PAPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/09/824,647
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,862
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/863,862
PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTING DATE: 1997-05-23
LENGTH: 14
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THER INFORMATION: Internal peptide of mouse GP88
OTHER INFORMATION: antisera against the GP88 used
OTHER INFORMATION: immunoaffinity step.
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1 Similarity 100.0%; Pred. No. 1.9e-06;
14; Conservative 0; Mismatches 0;
                 Sequence 5, Application US/09824647 Publication No. US20020183270A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 14; Conserva
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US-09-824-647-5
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Sequence 5, Application US/10218509 Publication No. US20030092661A1 GENERAL INFORMATION:

us-09-824-647-5.rapb

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; OTHER INFORMATION: (1)..(14); OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the COTHER INFORMATION: antisera against the GP88 used in the GPHER INFORMATION: immunoaffinity step.
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APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 2996.488/P001-A
CURRENT APPLICATION NUMBER: US/09/824,807
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1997-12-16
PRIOR FILING DATE: 1997-05-23
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                                                    TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
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Pred. No. 1.9e-06;
; Mismatches 0;
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Pred. No. 1.9e-06;
; Mismatches 0;
                             APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWT
FILE REFERENCE: 2996.488/P001-A
CURRENT APPLICATION NUMBER: US/09/813,156
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR PELLING DATE: 1997-12-16
PRIOR PELLING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09824807 Patent No. US20020094966A1
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SEQ ID NO 5 ELENGTH: 14
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Patentin Ver. 2.0
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Best Local Similarity 100.0
Matches 14; Conservative
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Best Local Similarity
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LENGTH: 14
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SOFTWARE:
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Publication No. US20030108950A1
GENERAL INFORMATION:
APPLICAMT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 2996.488/P001-A
CURRENT APPLICATION UNDER: US/10/281,160
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION UNDER: US/08/991,862
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 08/08/3,862
APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REPERENCE: 2996.488/P001-A
CURRENT APPLICANION NUMBER: US/10/218,509
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-05-23
NUMBER: OF SEQ ID NOS: 17
SOFTWARE: PATENTINY OF SEQ ID NOS: 17
SOFTWARE: PATENTINY OF SEQ ID NOS: 17
SOFTWARE: 144
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OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the OTHER INFORMATION: antisera against the GP88 used in the OTHER INFORMATION: immunoaffinity step.
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100.0%; Score 73; DB 9; Best Local Similarity 100.0%; Pred. No. 1.9e-06; Matches 14; Conservative 0; Mismatches 0;
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; Patent No. US20020061859A1
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NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
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ORGANISM: mouse granulin
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NUMBER OF SEQ ID NOS: 17
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LENGTH: 589
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GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
TILL OF INVENTION:
FILE REFERENCE: 2996.488/P001-A
CURRENT PAPLICATION NUMBER: US/09/824,647
CURRENT FILING DATE: 2001-04-04
FRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17
FRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23
FRIOR FILING DATE: BALLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
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TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILLE REFERENCE: 29996.488/POOL1-A
CURRENT APPLICATION NUMBER: US/10/218,509
RICOR APPLICATION NUMBER: 08/991,862
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1997-05-23
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Publication No. US20030108950A1
GENERAL INFORMATION:
APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001.A
CURRENT APPLICATION NUMBER: US/10/281,160
CURRENT FILING DATE: 2002-10-28
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PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 08/863,862
PRIOR FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Mouse epithelin/granulin
US-10-218-509-2
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Publication No. US20030092661A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.0
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LENGTH: 589
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APPLICANT: Serrero, Ginette
TILE OF INVENTION: 88 AD TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 2996.488/P001-A
CURRENT PILICATION NUMBER: US/09/813,156
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1997-12-16
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APPLICANT: Serrero, Ginette
APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 ROA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-8
CURRENT APPLICATION NUMBER: 08/991,862
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1997-12-16
PRIOR FILING DATE: 1997-05-23
PRIOR FILING DATE: 1997-05-23
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                                                                                                                                        100.0%; Score 73; DB 9; Length 589; 100.0%; Pred. No. 9e-05;
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                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 08/863,862
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin yer. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Mouse epithelin/granulin
US-09-824-807-2
                                                                      ; TYPE: PRT
; ORGANISM: Mouse epithelin/granulin
US-10-281-160-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mouse epithelin/granulin
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09813156 Patent No. US20020061859A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09824807
Patent No. US20020094966A1
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562 SARGTKCLRKKIPR 575
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 589
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
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Best Local Similarity 100.

Matches 14; Conservative
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Best Local Similarity 100.
Matches 14; Conservative
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Matches 14; Conservative
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3 RGTKCLRKKIPR 14
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ORGANISM: Human granulih
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Matches 9; Conserv
                                                      GENERAL INFORMATION:
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OTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/09824647
Publication No. US20020183270A1
GENERAL INFORMATION:
APPLICANT: Serrero, Ginette
TITLE OF INFORTION: 88 KDA TUMORICENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/FD011-A
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,862
PRIOR PILING DATE: EARLIER FILING DATE: 1998-08-17
PRIOR PLING DATE: EARLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 10 NOS: 2.0
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INFORMATION:
CURRENT RELIGION:
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: CT/VS00/05882
PRIOR APPLICATION NUMBER: CT/VS00/05882
PRIOR PILING DATE: 1000-03-08
PRIOR PILING DATE: 1099-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10; Length 621;
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Pred. No. 0.0066;
2; Mismatches 1; Indels
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Pred. No. (
                                                                                                                               Sequence 1416, Application US/09925301
Patent No. US20020052308A1
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ilarity 75.0%;
Conservative
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1 SARGTKCLRKKIPR 14
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1416
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Best Local Similarity
Matches 9; Conserv
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LENGTH: 14
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RESULT 15

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APPLICANT: Serrero, Ginette
TITLE OF INFORMATION:
TITLE OF INFORMATION:
FILE REFERENCE: 29996.488/P001-A
CURRENT FILITG DATE: 2002-10-28
PRIOR APPLICATION NUMBER: US/08/991,862
PRIOR PILING DATE: 1998-08-17
PRIOR PILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VOIL: 2.0
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OTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody.
                                                                     APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 RDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/10/218,509
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR PPLICATION NUMBER: 08/981,862
PRIOR PLICATION NUMBER: 08/863,862
PRIOR PLILING DATE: 1998-08-17
PRIOR PLILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)..(14).
OTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody.
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Pred. No. 0.0066;
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Pred. No. 0.0066;
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Publication No. US20030108950A1
Sequence 7, Application US/10218509
Publication No. US20030092661A1
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75.08;
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75.0%;
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SEQ ID NO 7
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Best Local Similarity 75.0
Matches 9; Conservative
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                                                        GENERAL INFORMATION:
APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFRENCE: 29996.488,P001-A
CURRENT TILING DATE: 2001-03-21
PRIOR PELICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1997-12-16
PRIOR FILING DATE: 1997-12-16
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 117
SOFTWARE: PATENTE 1997-05-23
NUMBER OF SEQ ID NOS: 12.0
SOFTWARE: PRI
OFFINE PRI
OFFINE PRI
OFFINE PRI
OFFINE PRI
OFFINE SEATURE

NAME/KET: PEPTIDE
CARTON: (1)...(14)
COTHER INFORMATION: Internal peptide of human GP88 monoclonal antibody.
US-09-813-156-7
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Pred. No. 0.0066;
2; Mismatches 1
US-09-813-156-7; Sequence 7, Application US/09813156; Patent No. US20020061859A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 72.6%;
Best Local Similarity 75.0%;
Matches 9; Conservative
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3 RGTKCLRKKIPR 14 |||||||::|| 3 RGTKCLRREAPR 14

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Search completed: July 8, 2003, 16:31:41 Job time: 14.641 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

(without alignments) 94.918 Million cell updates/sec July 8, 2003, 16:19:45; Search time 14.1795 Seconds Run on:

US-09-824-647-5 Perfect score: Title:

73 1 SARGTKCLRKKIPR 14 Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

2: pir2:* 3: pir3:* 4: pir4:* PIR_73:4 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	epithelin/qranulin	epithelin/granulin	granulin precursor	hypothetical prote	Down syndrome crit	glutamine-tRNA lig	hypothetical prote	hypothetical prote	poly(A) polymerase	probable aminotran	serine/threonine-p	hypothetical prote	hypothetical prote		hypothetical prote	hypothetical prote		phosphoglucomutase	dueuine tRNA-ribos	phosphoglucomutase	phosphoglucomutase	hypothetical prote	hypothetical prote		sterol 0-acyltrans	hypothetical prote	SINAH1 protein [im	integrase, phage f	diacylglycerol 0-a
		ដ	C38128	B38128	GYHU	G64476	JC7279	AB0321	T24824	E64450	875598	AH0361	T48400	T02518	C86246	C71554	T49514	T28023	T49513	AE3057	D64354	AH3487	A96229	T19416	.F97737	B82299	T01294	S60947	T50560	B82272	H84576
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æ	Query	Match	100.0	89.0	79.5	56.2	54.8	54.8	53.4	53.4	53.4	52.1	52.1	52.1	51.4	50.7	50.7	50.7	50.7	50.7	50.7	.20.7	50.7	50.0	49.3	49.3	49.3	49.3	49.3	49.3	49.3
		Score	73	65	28	41	40	40	39	39	39	38	38	38	37.5	37	37	37	37	37	37	37.	37	36.5	36	36	36	36	36	36	36
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B95135	D98003	T52584	T40036	T45908	A82543	873679	н97253	148141	C47538	T33983	164021	T19253	A37055	T03960	T24810	
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453	453	520	803	839	1167	1300	162	591	41	141	167	233	270	343	350	
49.3	49.3	49.3	49.3	49.3	49.3	49.3	48.6	48.6	47.9	47.9	47.9	47.9	6.44	47.9	47.9	
36	36	36	36	36	36	36.	35.5	35.5	35	32	35	35	35	35	35	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

Particle of the procurs of the procurs of the procession of the pr A; Accession: C38128

A; Residues: 1-589 <-PLO.
A; Residues: 1-589 <-PLO.
A; Residues: 1-589 <-PLO.
A; Cross-references: GB:X62321; NID:950851; PIDN:CAA44197.1; PID:950852
R; Baba, T.; Nemoto, H.; Watanabe, K.; Arai, Y.; Gerton, G.L.
FEBS Lett. 322, 89-94, 1993
A; Title: Exon/Intron organization of the gene encoding the mouse epithelin/granul
A; Reference number: S32503; MUID:99245991; PMID:8482392

A; Molecule type: DNA A; Moeleus: 18-349, L',351-589 <BAB> R; Readues: 18-349, L',351-589 <BAB> R; Redues, T.; Hofff, H.B. Mol. Reprod. Dev. 34, 233-243, 1993 Mol. Reprod. Dev. 34, 233-243, 1993 Mol. Reprod. Dev. 34, 233-243, 1993 Mol. Reference number: 148141; MUID:93228994; PMID:8471244 A; Accession: 149468

A, Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA

A; Residues: 1-250, L', 252-253, VV, 255-349, LV, 351-401, 'SA', 404-589 <RES>
A; Cross-references: GB:M86736; NID:9191766; PIDN:AAA37191.1; PID:9191767
B; Zhou, J.; Gao, G.; Crabb, J.W.; Serrero, G.
Blol. Chem. 268, 10863-10869, 1993
A; Title: Purification of an autocrine growth factor homologous with mouse epithel A; Reference number: A46705; MUID:93266526; PMID:8496151

A; Status: preliminary

A; Molecule type: protein A; Residues: 18-19,'X',21-25,'X',27-29,'XX',32;'XXX',119-127;152-154,'DXK',158-161 C; Superfamily: granulin

Length 589; 0; Indels 100.0%; Score 73; DB 2; 100.0%; Pred. No. 2e-05; ive 0; Mismatches 0 Query Match 100. Best Local Similarity 100. Matches 14; Conservative

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Gaps

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RESULT B38128

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A;Residues: 11406, R, 408-433, G', 435-453, G', 455-459, Q', 461-546, A', 548-566, R', 5
A;Cross-references: GB:M'5161; NID:g183612; PIDN:AAA58617.1; PID#g183613
A;Note: this sequence has been revised in reference JC1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Map position: 17pter-17gter
Introns: 46/3; 88/3; 117/1; 154/3; 200/1; 236/3; 279/1; 311/3; 393/3; 471/3; 548,
                                        Proc. Natl. Acad. Sci. U.S.A. 89, 1715-1719, 1992
A;Title: Isolation and sequence of the granulin precursor cDNA from human bone marr
A;Reference number: A38118; MUID:92179253; PMID:1542665
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R; Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Bl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: protein
Residues: 442-446, XDTSS', 456-458, DG' <BA4>
Residues: 442-446, XDTSS', 456-458, DG' <BA4>
Rardana, A.; Bagshawe, K.D.; Coles, B.; Read, D.; Taylor, M.
c. J. Cancer 67, 686-692, 1993
Title: Characterisation of UGP and its relationship with beta-core fragment.
Reference number: A56873; MUID:93229246; PMID:8471426
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C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 29-Sep-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: protein
Residues: 206-218, H, 220-233 <BA2>
Note: this protein was purified and characterized as granulin
Accession: C36698
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Residues: 364-367, 'X',369-385,'H',387-396 <BA3>
Note: this protein was purified and characterized as granulin
Accession: D36698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: this protein was purified and characterized as granulin Accession: B36698
                                                                                                                                                                                                                                                                                                                            R;Bateman, A.; Belcourt, D.; Bennett, H.; Lazure, C.; Solomon, Blochem. Blophys Res. Commun. 173, 1161-1168, 1990 A;Title: Granulins, a novel class of peptide from leukocytes. A;Reference numbér: A36698; MOID:91097544; PMID:2268320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: protein
kesidues: 281-283, XY,285-289, SZ,291-295 KRAR>
keperimental source: urine
hote: sequence extracted from NCBI backbone (NCBIP:129524)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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06-261/Product: granulin B *status experimental <GRB>
81-336/Product: granulin A *status experimental <GRB>
64-417/Product: granulin C *status experimental <GRC>
42-496/Product: granulin D *status predicted <GRD>
18-573/Product: granulin E *status predicted <GRE>
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18-593/Product: progranulin #status predicted <PRO>
18-44/Product: paragranulin #status experimental <PGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <SIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       granulin G #status predicted <GRG>
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              Bateman, A.
1715-1719, 1992
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: GDB:136006; OMIM:138945
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Keywords: glycoprotein; tandem repeat
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566 AARGTKCLRREAPR 579
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Matches 10; Conservative
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Residues: 281-336 <BAT>
                                                                                                                                                                                      A; Molecule type: mRNA
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N;Alternate names: epithelin
C;Cortains: granulin A; granulin B; granulin C; granulin D; granulin B; granulin F; gran
C;Specias: Homo saplens (man)
C;Date: 30-Sep-1992 #sequence_revision 03-May-1996 #text_change 08-Dec-2000
C;Accession: JC1284; A38128; A38118; A36698; B36698; C36698; D36698; A56873
R;Bhandari, V.; Bateman, A.
epithelin/granulin precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 20-Aug-1999
C;Accession: B38128; A36199; B36698; E36698; E3272
R;Plowman, G.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Todaro, G.J
A;Tille: The epithelin precursor encodes two proteins with opposing activities on epithe A;Reference number: A38128; MUID:92317004; PMID:1618805
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A; Title: The epithelin precursor encodes two proteins with opposing activities on epithe A; Reference number: A38128; MUID:92317004; PMID:1618805
                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:X62322; NID:956108; PIDN:CAA44198.1; PID:956109
R;Shoyab, M.; McDonald, V.L.; Byles, C.; Todaro, G.J.; Plowman, G.D.
Proc. Natl. Acad. Sci. U. S.A. 87, 7912-7916, 1990
A;Title: Epithelins 1 and 2: isolation and characterization of two cysteine-rich growth-A;Reference number: A36199; MUID:91045907; PMID:2236009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: The complementary deoxyribonucleic acid sequence, tissue distribution, and cell
A;Reference number: I53272; MUID:94062640; PMID:8243292
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A;Cross-references: GB:M97750; NID:g204223; PIDN:AAA16903.1; PID:g204224
C;Superfamily: granulin
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A; Title: Structure and chromosomal location of the human granulin gene.
A; Reference number: JC1284; MUID:93038704; PMID:1417868
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A;Residues: 1-593 <PLO>
A;Cross-references: GB:X62320; NID:g31192; PIDN:CAA44196.1; PID:g31193
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A;Residues: 279-307,'SB',310-324,'T',326,'X',328,'Q' <BAT>
R;Bhandari, V.; Giaid, A.; Bateman, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 173, 1161-1168, 1990
A;Title: Granulins, a novel class of peptide from leukoc
A;Reference number: A36698; MUID:91097544; PMID:2268320
A;Accession: E36698
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Endocrinology 133, 2682-2689, 1993
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A;Residues: 280-300 <SHO>
A;Accession: B36199
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A;Residues: 205-226 <SH2>
R;Bateman, A.; Belcourt, I
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A; Molecule type: DNA
A; Residues: 1-59 <BHA>
R; Plowman, G.D.; Green, J
J. Biol. Chem. 267, 13073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 12; Conserv
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A; Residues: 1-589 <PLO>
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Matches
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C; Accession: E64450
R; Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Relch, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Reich, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Gloc science 273, 1058-1073, 1996
A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; I A; Tile: Complete genome sequence of the methanogenic archaeon, Methanococcus jan A; Reference number: A64300; MUID:96337999; PMID:8688087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL: 272515; PIDN: CAA96685.1; GSPDB: GN00023; CESP:T11A5.5
A; Experimental source: clone T11A5
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C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein TilA5.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct<sup>4</sup>1999 #text_change 15-Oct-1999
C;Superfamily: glutamine-tRNA ligase; glutamine-tRNA ligase homology
C;Reywords: ligase
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                                                                                             Length 555;
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A;Start codon: GTG
C;Superfamily: conserved hypothetical protein MJ1206
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Pred. No. 19;
1; Mismatches
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                                                                                       Score 40; DB 2
Pred. No. 22;
0; Mismatches
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submitted to the EMBL Data Library, May 1996
A;Reference number: Z19939
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                                                                                       Query Match 54.8%;
Best Local Similarity 72.7%;
Matches 8; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                                                                2 ARGTKCLRKKI 12
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A; Introns: 202/2
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Best Local S
Matches 7
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A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Reference number: AB0001; MUID:21470413; PMID:11586360
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Schon, J.D.; Sadow, P. W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A.; A; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschli A; Reference number: A64300; MUID:96337999; PMID:8688087
A; Accession: G64476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Vidal-Taboada, J.M.; Lu, A.; Pique, M.; Pons, G.; Gil, J.; Oliva, R. Biochem. Biophys. Res. Commun. 272, 156-163, 2000 A;Title: Down syndrome critical region gene 2: Expression during mouse development and A;Reference number: JC7279 A;Accession: JC7279
                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA Residues: 1.452 <BUL>
A;Residues: 1.452 <BUL>
A;Cross-references: GB:U67582; GB:L77117; NID:g1592064; PIDN:AAB99426.1; PID:g1500295;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GB: AL590842; PIDN: CAC92873.1; PID: 915980617; GSPDB: GN00175
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Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 21
C;Superfamily: human 32.9K leucine-rich protein (chromosome 21)
C;Keywords: Down's syndrome; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 2; Length 289;
Pred. No. 13;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 56.2%; Score 41; DB 2; Length 452; Best Local Similarity 87.5%; Pred. No. 12; Matches 7; Conservative 1; Mismatches 0; Indels.
                                                                                                                                                                                                                                                                                                                                                             A;Map position: REV1378352-1376994
C;Superfamily: conserved hypothetical protein MJ1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Species: Mus musculus (house mouse)
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Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 KCLRKKIP 13
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A; Residues: 1-289 <VID>
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A; Residues: 1-555 <KUR>
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A;Gene: glnS
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R;Kieber, J.J.; Rothenberg, M.; Roman, G.; Feldmann, K.A.; Ecker, J.R. Cell 72, 427-441, 1993.
A;Title: CTR1, a negative regulator of the ethylene response patimay in Arabidopsis A; Contents: Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein At2937520 [imported] - Arabidopsis thaliana
N.Alternate names: hypothetical protein F13M22.2
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001
C;Accession: T02518; G84793
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sy submitted to the EMBL Data Library, June 1998
A;Bescription: Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence.
A;Reference number: 214677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C
K;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, M.; VanAken, S.E.; Umayam, L.; Tailc
euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vent
                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 5
A;Introns: 216/3; 317/2; 364/3; 399/2; 468/1; 560/1; 573/3; 596/3; 630/2; 658/3; 69
A;Note: F17C15.150
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase h
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Affilie: Sequence and analysis of chromosome 2 of the plant Arabidopsis thallana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: G84793
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                                                                                                       A; Experimental source: cultivar Columbia; BAC clone F17C15
R; Kieber, J.J.; Rothenberg, M.; Roman, G.; Feldmann, K.A.; Ecker, J.R.
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                                                                                                                                                                                                                                                                                                          A; Status: preliminary; not compared with conceptual translation
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A;Residues: 1-825 <ROU>
A;Cross-references: EMBL:AC004684; NID:93236234; PID:93236235
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Pred. No. 74;
2; Mismatches
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Pred. No. 74;
3; Mismatches
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50.0%;
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57.1%;
                                                                                      A; Cross-references: EMBL: AL162506
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Best Local Similarity 50.0
Matches 6; Conservative
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A; Residues: 1-468,470-821
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Best Local Similarity
'-has 8; Conserva
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-821 <BEV>
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F; 549-812/Domain
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K; Raneko, T.; Stot, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:D90912; GB:AB001339; NID:g1653228; PIDN:BAA18159.1; PID:d101889
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 17-Nov-2000
C;Accession: T48400; A45178
R;Bevan, M.; Pohl, T.; Welzenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, Isubmitted to the Protein Sequence Database, March 2000
A;Reference number: 224492
A;Accession: T48400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB: AL590842; PIDN: CAC92219.1; PID: 915980931; GSPDB: GN00175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999 C;Accession: S75598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Length 942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                   poly(A) polymerase - Synechocystis sp. (strain PCC 6803) N;Alternate names: protein s111253
                                                                                                                                                                                                                                                                                                                                                           A; Reference number: S74322; MUID:97061201; PMID:8905231
A; Accession: S75598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 54;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38; DB
Pred. No. 40;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C,Genetics:
A,Gene: YPO2975
C,Superfamily: aspartate transaminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 52.1%;
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::|| |||:|| || || 72 TSRGIPCLRRAISR 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SARGTKCLRKKIPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             865 AARGNKLLRKQI 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SARGTKCLRKKI 12
                                                                                                             C; Species: Synechocystis sp. A; Variety: PCC 6803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-942 <KAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-411 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: AH0361
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26

Gaps

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Length 327;

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A,Cross-references: EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.660
A,Experimental source: BAC clone B14D6; strain OR74A
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                                                                                                                                                                                                                                                                                                          DB 2;
50;
                                                                                                                                                                                                                                                                                                       Score 37; DB 2
Pred. No. 50;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8, 2003, 16:29:27
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            276 RGPQCLRRRPP 286
                                                                                                                                                                                                                                                                                                                                                                                                                       3 RGTKCLRKKIP 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: July
Job time: 16.1795 secs
                                                                                                                   A; Residues: 1-327 <SCH>
                                                                                                                                                                                              C;Genetics:
A;Gene: NCSP:B14D6.660
A;Map position: 6
                                                               A;Status: preliminary
                                                                                            A; Molecule type: DNA
                                     ; Accession:
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                                                                                                                                                                                                                                                   R;Theologis, A.; Ecker, J.R.; Falm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
Mature 408, 816-820, 2000
Mature 408, Sicher, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: T49514
R;Schulte, U.; Algn, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE001286; GB:AE001273; NID:g3328516; PIDN:AAC67718.1; PID:g332855
A;Experimental source: serotype D, strain UW-3/Cx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac
A;Reference number: A71570; MUID:990000809; PMID:9784136
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     orobable polysaccharide hydrolase - Chlamydia trachomatis (serotype D, strain UW3/Cx)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Chlamydia trachomatis
.Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Neurospora crassa
:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
                                                                                                                                                                                              #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; S
Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 341;
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Pred. No. 44;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                     hypothetical protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #tex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37.5; Di
Pred. No. 42;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Wolecule type: DNA
A;Residues: 1-283 <ARN>
A;Cross-references: GB:AE001286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|| ||||||:
186 KGTITSKCLRKKV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 RGT---KCLRKKI 12
802 KGTSMLEKKVPK 813
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Best Local Similarity 45.5
Matches 5; Conservative
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157 GGRCIHKQLPR 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 282, 754-759, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-341 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: C71554
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

July 8, 2003, 16:16:30; Search time 6.82051 Seconds (without alignments) 85.136 Million cell updates/sec Run on:

US-09-824-647-5 73 1 SARGTKCLRKKIPR 14 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	20000	Describeron	핕	н	P28799 h granulins	08zdd9 yersinia pe	P81534 homo sapien	-	Q8veel mus musculu	Q44603 buchnera ap	arabidops	P39671 agrobacter1	Q57878 methanococc		P75296 mycoplasma		-			_		ara		P47934 mus musculu	,	Q9kkq7 vibrio chol	P08638 saccharomyc	Q28628 oryctolagus	•	P33467 feline ente		E	P07772 a c1s-1,2-d	P38232 saccharomyc	Q64299 mus musculu
SUMMAKIES	ć.	77	GRN_MOUSE	GRN_RAT	GRN_HUMAN	SYQ_YERPE	BD03_HUMAN	YC06_METJA	LMC1_MOUSE	TRPC_BUCSC	CTR1_ARATH	PGMU_AGRTU	Y436_METJA	DRTS_TRYBB	Y338_MYCPN	DPOL_THEHY	GRN_CAVPO	BAXC_HUMAN	YFCN_HAEIN	RL7_MOUSE	CYAA_STIAU	ALG6_ARATH	KU70_MOUSE	CACP_MOUSE	PTMA_BUCAI	PTMA_VIBCH	LEUR_YEAST	AKA9_RABIT	RK28_CYAPA	V6B_CVFE3	RECR_TREPA	KGUA_MYCTU	BEND_ACICA	REG2_YEAST	NOV_MOUSE
	2	9 :	-	-	٦	-	-	~	Н	Н	Н	-	-	-	-	~	-	-		-		-	-	-	-	-	Н	₫	-	Н		-		-	-
	. 4	reng cu	589	288	593	555	67	424	365	461	821	543	550	527	1300	1668	591	41	167	270	424	533	608	627	632	649	886	1087	. 70	176	201	208	261	338	354
æ	Query		100.0	89.0	79.5	54.8	53.4	53.4	52.1	52.1	52.1	50.7	50.7	49.3	49.3	49.3	48.6	47.9	47.9	47.9	47.9	47.9	47.9	47.9	47.9	47.9	47.9	47.3	46.6	46.6	46.6			46.6	46.6
	01000	3000	73	65	28		39	39	38	38	38	37	37	36	36	36	35.5	32	35	35	32	35	35	35		35	35	34.5	34	34	34	34	34	34	34
	Result		1	6	e	4	2	9	7	80	6	10	11	12	13.	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33

P48745 homo sapien	Q9uyv6 pyrococcus	Q97pr0 streptococc	Q9kta6 vibrio chol	P57847 pasteurella	Q03162 saccharomyc	Q9cly8 pasteurella	058446 methanococc	057472 brachydanio	000339 homo sapten	008746 mus musculu		
NOV_HUMAN	Y927_PYRAB	SYN_STRPN	SYO_VIBCH	SYQ_PASMU	YMZ0_YEAST	PTMA_PASMU	RPA2_METJA	CHRD_BRARE	MTN2_HUMAN	MTN2_MOUSE	POL_HV1EL	
Н	Н	Н	-	, -1	Н	-	-	Н	Н	Н	7	
357	405	447	556	559	620	624	859	940	926	926	1002	
46.6	46.6	46.6	46.6	46.6	46.6	46.6	46.6	46.6	46.6	46.6	46.6	
34	34	34	34	34	34	34.	34	34	34	34	34	
34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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-!- FUNCTION: GRANULINS HAVE POSSIBLE CYTOKINE-LIKE ACTIVITY. THEY MAY PLAY A ROLE IN INFLAMMATION, WOUND REPAIR, AND TISSUE REMODELING.
-!- TISSUE SPECIFICITY: UBLOUTOUS; MOST ABUNDANT IN THE SPLEEN AND SEVERAL TISSUES OF ENDOCRINE SIGNIFICANCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plowman G.D., Green J.M., Neubauer M.G., Buckley S.D., McDonald V.L., Todaro G.J., Shoyab M.;
"The epithelin precursor encodes two proteins with opposing activities on epithelial cell growth.";
J. Biol. Chem. 267:13073-13078(1992).
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Granulins precursor (Acrogrania) [Contains: Granulin 1 (Granulin G);
Granulin 2 (Granulin F); Granulin 3 (Granulin B) (Epithelin 2);
Granulin 4 (Granulin A) (Epithelin 1); Granulin E)].
Granulin 6 (Granulin D); Granulin 7 (Granulin E)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                            ..) (POTENTIAL)...) (POTENTIAL)...) (POTENTIAL)...)
                                                                                 · · · ( POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 204-225 AND 279-299.

MEDLINE-91045907; PubMed-2236009;
Shoyab M., McDonald V.L., Byles C., Todaro G.J., Plowman G.D.;
"Epithelins 1 and 2: isolation and characterization of two
cysteine-rich growth-modulating proteins.";
Proc. Natl. Acad. Sci. U.S.A. 87:7912-7916(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               distribution, and cellular localization of the rat granulin
                                                                                                                                                                                           100.0%; Score 73; DB 1; Length 589; 100.0%; Pred. No. 9e-06;
                                                                                                                                                                                                                            0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bateman A., Belcourt D.R., Bennett H.P., Lazure C., Sold "Granulins, a novel class of peptide from leukocytes."; Biochem. Biophys. Res. Commun. 173:1161-1168(1990).
                                                                                                                                                               1DE8229C413CB787 CRC64;
GRANULIN 3.
GRANULIN 4.
GRANULIN 5.
GRANULIN 5.
GRANULIN 7.
N-LINKED (GLCNAC. .
N-LINKED (GLCNAC. .
N-LINKED (GLCNAC. .
N-LINKED (GLCNAC. .
                                                                                                                                                REF.
                                                                                                                                                                                                                                                                                                                                                                         588 AA.
                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bhandari V., Giaid A., Bateman A.; "The complementary deoxyribonucleic acid
                                                                                                                                                -> R (IN
                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endocrinology 133:2682-2689(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-94062640; PubMed-8243292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92317004; PubMed-1618805;
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                                                                                                                                                               63458 MW;
                                                                                                                                                                                                                                                                            562 SARGTKCLRKKIPR 575
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                                                                                                                                                                                                          Local Similarity 100.
es 14; Conservative
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                                                                                                                                                             589 AA;
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(Rel.
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by anon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sfb.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRELHUMAN STANDARD; PRT; 593 AA.
P28799; P23781; P23783; P23784; Q9BWE7;
D1-NOV-1991 (Rel. 20, Created)
O1-NOV-1991 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Granulins precursor (Acrogranin) [Contains: Paragranulin; Granulin 1 (Granulin 2; Granulin 2; Granulin 5; Granulin 5; Granulin 5; Granulin 7; Granulin 6; Granulin 8); Granulin 7 (Granulin 8); Granulin 7 (Granulin 8);
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Bhandari V., Palfree R.G.E., Bateman A.;
Isolation and sequence of the granulin precursor cDNA from human bone marrow reveals tandem cysteine-rich granulin domains.";
Proc. Natl. Acad. Sci. U.S.A. 89:1715-1719(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
S -> FP (IN REF. 2).
TK -> SB (IN REF. 4).
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Pred. No. 0.00026;
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(IN REF. 2
-1- PTM: GRANULINS ARE DISULFIDE BRIDGED.
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PSO0799; GRANULINS; 7.
; Repeat; Glycoprotein;
                                                                                                                                                                   PIR; A36199; A36199.
PIR; B36199; B36199.
PIR; E36698; E36698.
INTERFO; IPR000118; Granulin.
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                                                                                                                                       EMBL; M97750; AAA16903.1; -. EMBL; X62322; CAA44198.1; -.
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Matches 12; Conservative
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588 AA;
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REVISIONS, SEQUENCE FROM N.A.

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                                                                   Plowman G.D., Green I.M., Neubauer M.G., Buckley S.D., McDonald V.L., Todaro G.J., Shoyab M.; The epithelin precursor encodes two proteins with opposing activities
        Bhandari V., Bateman A.; "Structure and chromosomal location of the human granulin gene."; Blochem. Blophys. Res. Commun. 188:57-63(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Signal; Alternative splicing;
                                                                                                                                                                                            Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                        Yu W., Glbbs R.A.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                              SEQUENCE OF 206-233; 281-336; 364-396 AND 442-447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACROGRANIN.
PARAGRANULIN.
GRANULIN 1.
GRANULIN 2.
GRANULIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch)
                                                                                                                                                                 SECUENCE FROM N.A. (ISOFORMS 1 AND 2).
TISSUE-Cervix, and Lung;
                                                                                            on epithelial cell growth.";
J. Biol. Chem. 267:13073-13078(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M75161; AAA58617.1; ALT_SEQ.
                                                   TISSUE-Kidney;
MEDLINE-92317004; PubMed-1618805;
MEDLINE-93038704; Pubmed-1417868;
                                                                                                                                                                                                                               MEDLINE-91097544; PubMed-2268320;
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EMBL; ARO55008; AAC05359.1; --
EMBL; BC000324; AARH00324.1; --
EMBL; BC010577; AAH10577.1; --
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PIR; D36698; D36698.
PIR; JC1284; JC1284.
Genew; HGNC:4601; GRN.
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                                            SEQUENCE FROM N.A.
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SIGNAL
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                     GRANULIN 7.

GRANULIN 7.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .).

N-LINKED (GLCNAC. . .).

MISSING (IN ISOFORM 2).
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
6]utaminyl-tRNA synthetase (EC 6.1.1.18) (Glutamine--tRNA ligase)
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(POTENTIAL).
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-1- SUBDINI: Monomer (By similarity).
-1- SUBCELLUIAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 58; DB 1; Length 593;
Pred. No. 0.005;
3; Mismatches 1; Indels
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W -> H (IN REF. 6).
4E402BDB16DE2819 CRC64;
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/FTId-VAR_003445
                               GRANULIN 5.
GRANULIN 6.
GRANULIN 4.
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InterPro; IPR000924; Glu_tRNA-synt_lc.
InterPro; IPR001412; tRNA-synt_I.
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PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
                            GRANULIN
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Matches 10; Conservative
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MIM; 606611;
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EMBL;
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TISSUE-KELALINOCYTES, TREACHEAL EPITHELIUM, and Lung epithelial cells; MEDLINE-21101950; PubMed-11085990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Garcia J.-R., Jaumann F., Schulz S., Krause A., Rodriguez-Jimenez J., Forssmann U., Adermann K., Kluver E., Vogelmeier C., Becker D., Hedrich R., Forssmann W.-G., Bals R.;
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Discovery of new human defensins using a genomics-based approach.";
Gene 263:211-218(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: EXHIBITS ANTIMICROBIAL ACTIVITY AGAINST GRAM-POSITIVE
BACTERIA S.ANGENG AND S.POGENES, GRAM MEGATIVE BACTERIA
P.AERGGINOSA AND E.COLI AND THE YEAST C.ALBICANS. KILLS
MULTIRESISTANT S.AUREUS AND VANCOMYCIN-RESISTENT E.FAECIOM. NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harder J., Bartels J., Christophers E., Schroeder J.-M.; Isolation and characterization of human deta-defensin-3, a novelhuman inducible peptide antibiotic.";
J. Biol. Chem. 276:5707-5713(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21125233; PubMed-11223260;
Jia H.P., Schutte B.C., Schudy A., Linzmeter R., Guthmiller J.M.,
Johnson G.K., Tack B.F., Mitros J.P., Rosenthal A., Ganz T.,
McCray P.B. Jr.;
                                                                                                                                                                                                                                                                                                                                    P81534; Q9NPP6;
16-OCT-2001 (Rel. 40, Last sequence update)
15-OUN-2002 (Rel. 40, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Beta-defensin 3 precursor (BD-3) (hBD-3) (befensin like protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Identification of a novel, multifunctional beta-defensin (human beta-defensin 3) with specific antimicrobial activity. Its interaction with plasma membranes of Xenopus cocytes and the induction of macrophage chemoattraction."; cell Tissue Res. 306:257-264(2001).
                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Adler D.A., Diamond G., Sheppard P., Holloway J., Presnell S., Jaspers S., Whitmore T., Fox B., Gosink J., Rixon M., Gao Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haldeman B., O'Hara P.; "EST and geomic database mining yield novel human and mouse beta-defensins."
                                                                                                                           DB 1; Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                   "KMSKS" REGION.
ATP (BY SIMILARITY).
AD3C68D6FB56C0B5 CRC64;
                                                                                                                                                                                                                                                                                                                      67 AA.
                                    "HIGH" REGION.
                                                                                                                                                            0; Mismatches
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                                                                                                                           Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                        PRT;
                                    34 44 "H
268 272 "K
271 271 AT
555 AA; 63750 MW;
                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                            8; Conservative
                                                                                                                                                                                                                  167 AEGTACLRAKI 177
                                                                                                                                                                                              2 ARGTKCLRKKI 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Human)
                                                                                                                         Query Match
Best Local Similarity
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                  Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                             DEFB3 OR BD3
                                                                                                                                                                                                                                                                                                                      BD03_HUMAN
                                                                                    SEQUENCE
                                                                    BINDING
                                                                                                                                                                                                                                                                                                     BD03_HUMAN
                                                                                                                                                                                                                                                                                      RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
SIGNIFICANT HEMOLYTIC ACTIVITY WAS OBSERVED.
--- SUBCELLULAR LOCATION: Secreted.
--- TISGUE SPECIFICITY: HIGHLY EXPRESSED IN SKIN AND TONSILS, AND TO A LESSER EXTENT IN TRACHEN, UTERUS, KIDNEY, THYMUS, ADENOID, PHARYNX AND TONGUE. LOW EXPRESSION IN SALIVARY GLAND, BONE MARROW, COLON, SYOMACH, POLLY AND LARYNX. ON EXPRESSION IN SMALL INTERINE.
--- INDUCTION: BY INFECTION OF BACTERIA AND BY INTERFERON GAMMA.
--- INDUCTION: BY INFECTION OF BACTERIA AND BY INTERFERON GAMMA.
--- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE-96337999; PubMed-8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Karlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoglagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
Compact genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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BY SIMILARITY.
BY SIMILARITY.
54266DE1C90D4B65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ); DB 1;
): 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 273:1058-1073(1996).
-!- SIMILARITY: BELONGS TO THE UPF0095 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     424 AA.
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Mismatches
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001855; Defensin_beta.
Pfam; PF00711; Defensin_beta; 1.
Antibiotic; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ237673; CAC03097.1; -. EMBL; AF295370; AAG02237.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seq
16-ocr-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AB037972; BAB40572.1;
AF301470; AAG22030.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7697 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SARGTKCLRKK 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
67
55
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Les 7; Conserv
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between

This

Query Match

ð a **08VEE1**;

LMCD1

LMC1 MOUSE

RESULT 7

SARGVACLRCK 32

22

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lai C.-Y. Baumann P., Moran N.A.;

"Genetics of the tryptophan blosynthetic pathway of the prokaryotic endosymbiont (Buchnera) of the aphid Schlechtendalia chinensis.";

"Genetics of the tryptophan blosynthetic pathway of the prokaryotic endosymbiont (Buchnera) of the aphid Schlechtendalia chinensis.";

"Insect Mol. Biol. 4:47-59(1995).

"CATALYZED BY THE ISOMERASE, CODED BY THE TREY PRACTION IS CATALYZED BY THE SYMPHANSE, CODED BY THE TREY DOMAIN; THE SECOND REACTION IS CATALYZED BY THE SYMPHASE, CODED BY THE TREY DOMAIN; THE SECOND C. C-CATALYZED BY THE SYMPHASE, CODED BY THE TREY DOMAIN; THE SECOND REACTION IS CATALYZED BY THE SYMPHASE, CODED BY THE TREY DOMAIN; THE CATALYZED BY THE SYMPHASE, CODED BY THE TREY DOMAIN; THE CATALYZED BY THE SYMPHASE, CODED BY THE TREY FAMILY.

"C-I- PATHWAY: Tryptophan blosynthesis; third step.

"I DATHWAY: Tryptophan blosynthesis; fourth step.

"I DATHWAY: Tryptophan blosynthesis; fourth step.

"I DATHWAY: TYPTOPHAN BLOSYNTHESIS; fourth step.

"I DATHWAY: TYPTOPHAN BLOSYNTHESIS; fourth step.

"I SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE TRPF FAMILY.
                                                                                                                                                                                                           Ju-MAY-2000 (Rel. 39, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Tryptophan biosynthesis protein trpCF [Includes: Indole-3-glycerol phosphate synthase (EC 4.1.1.48) (1695); N-(5'-phosphorintary) ribosyl)anthranilate isomerase (EC 5.3.1.24) (PRAI)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rryptophan biosynthesis; Isomerase; Lyase; Multifunctional enzyme;
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Pred. No. 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Buchnera aphidicola (subsp. Schlechtendalia chinensis)
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        821 AA.
                                                                                                                                                         461 AA
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                                                                                                                                                         PRT;
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75.0%;
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InterPro; IPR001240; PRAI.
Pfam; PF00018; IGPS; 1.
ProDom; PF00057; PRAI; 1.
ProDom; PF00151; IGPS; 1.
PROSITE; PS00614; IGPS; 1.
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Best Local Similarity 75.0.
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                                                                                                                                                         STANDARD;
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461
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346 CLKKKIPK 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=118110;
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                                                                                                                                                         TRPC_BUCSC
Q44603;
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                                                                                                                           TRPC_BUCSC
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셤
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                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                              SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                  EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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Pred. No. 14;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 1; Length 424;
Pred. No. 11;
0; Mismatches 1; Indels
                                                            the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                          InterPro: IPR002936; DNAprim_toprim.
Pfam; PF01751; Toprim; 1.
SNART; SN00493; TOPRIM; 1.
Hypotherical protein; Complete proteome.
SEQUENCE 424 AA; 47388 MW; C55EC7A05B0CB2C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         365 AA; 40996 MW; DB8AA836364E47D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
LIN and cysteine-rich domains protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS004'8; LIM_DOMAIN_1; 2.
PROSITE; PS50023; LIM_DOMAIN_2; 2.
LIM domain; Metal-binding; Zinc; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . . LIM 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIM 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC019124; AAH19124.1;
InterPro; IPR001781; LIM.
Pfam; PF00412; LIM; 2.
ProDom; PD000094; LIM; 2.
                                                                                                                                                                                                                                                                                        EMBL; U67562; AAB99210.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.1%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 72.1.
Best Local Similarity 72.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMCI_MOUSE STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SARGTKCLRKK 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259 KCLRSKIP 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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SEQUENCE

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DOMAIN

DOMAIN

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Gaps

Si.

Transferase; Serine/threonine-protein kinase; ATP-binding.

POLY-GLY

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1. PROSITE; PS00108; PROTEIN_KINASE_ST; 1. PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

Pfam; PF00069; pkinase; 1. ProDom; PD000001; Euk_pkinase; 1. SMART; SM00221; STYKc; 1.

Pfam; PF00069;

PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).

578

BINDING

DOMAIN NP_BIND

DOMAIN DOMAIN

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REAL STRAIN—CV. Columbia,

REAL STRAIN—CV. Columbia,

REAL TADGE STRAIN—CV. Columbia,

REAL TADGE STRAIN—CV. Columbia,

REAL TADGE S. Kaneko T., Nakamura T., Hosouchi T., Kawashima K.,

RA Makazaki N., Natuono M., Matsuno A., Muraki A., Nakayama S.,

RA Nakazaki N., Natuono K., Okumura S., Shinpo S., Takeuchi C., Wada T.,

RA Matanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M.,

RA Huang E., Spiegel L., Gnol L., O'Shaughnessy A., Preston R.,

RA Huang E., Spiegel L., Gnol L., O'Shaughnessy A., Preston R.,

RA Belter E., Cordum H., Cordes M., Courtney W., Dante M.,

RA Stoneking T., Pepin K., Spieth J., Sekhon M., Armstrong J., Becker M.,

RA Belter E., Cordum H., Cordes M., Courtney W., Dante M.,

RA Belter E., Cordum H., Cordes M., Courtney W., Dante M.,

RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strowmatt C.,

RA Magner-McPherson C., Wollam A., Yoakum M., Bell M., Dedhia N.,

RA Mattenssen R., McCombe W.R., Wilson R.R., Mulber B., Marra M.,

RA Mattenssen R., McCombe W.R., Wilson R.K., Mulphy G., Bancroft I.,

RA Mattenssen R., McCombe W.R., Wilson R.K., Mulphy G., Bancroft I.,

RA Manperger G., Wedler H., Balke K., Wedler E., Johnson S.,

RA Richonson T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S.,

RA Weitzenegger T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S.,

Redpanser M., Lanberth S., Villarroel R., Gielen J., Ardiles W.,

RA Schueller C., Zaccaria P., Mewes H.-W., Bevan M., Fransz P., Fr

Ra Schueller C., Zaccaria P., Mewes H.-W., Bevan M., Fransz P. Fr

Fra Hallan R.

RA Schueller C., Saccaria P., Mewes H.-W., Bevan M., Fransz P. Fr

Fra Hallan R.

RA Fallan R.

RA Fallan R.

RA Fallan R.

RA Schueller C., Saccaria P., Mewes H.-W., Bevan M., Fransz P. Fr

Fra Hallan R.

RA Fallan R.
                                                                                                                                                                                                                                                                      SECURNCE FROM N.A.
STRAIN=cv. Columbia; TISSUE-Seedling;
MEDLINE-93161417; PubMed-8431946;
MEDLINE-93161417; PubMed-8431946;
Kieber J.J., Rothenberg M., Roman G., Feldmann K.A., Ecker J.R.;
"CTR1, a negative regulator of the ethylene response pathway in Arabidopsis, encodes a member of the raf family of protein kinases.";
Cell 72:427-441(1993).
                                                                                              CTR1 OR AF5G03730 OR F17C15_150.

Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis:

NCBI_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
TISSUE SPECIFICITY: EXPRESSED IN BOTH SEEDLINGS AND ADULT PLANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISCELLANEOUS: CTRI MUTANTS DISPLAY ETHYLENE-TREATED PHENOTYPES, RESULTING IN PLANTS WITH SMILL, UNEXPANDED LEAVES AND WHOSE SEED COTYLEDON GROWTH IS IMPAIRED.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
MIL/RAF SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              · I - FUNCTION: ACTS AS A NEGATIVE REGULATOR IN THE ETHYLENE RESPONSE
                          01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Serine/threonine-protein kinase CTR1 (EC 2.7.1.37).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 408:823-826(2000).
  (Rel. 32,
(Rel. 32,
(Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
01-NOV-1995
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PATHWAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L08789; AAA32779.1; -
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InterPro; IPR000719; Euk_pkinase. InterPro; IPR004040; STY_pkinase. InterPro; IPR002290; Ser_thr_pkin

AL162506; CAB82938.1;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agrobacterium tumefaciens.";
J. Bacteriol. 172:1640-1646(1990).
-!- FUNCTION: THIS ENTYME PARTICIPATES IN BOTH THE BREAKDOWN AND
-SYNTHESIS OF GLUCOSE. REQUIRED FOR THE SYNTHESIS OF CAPSULAR
POLYSACCHARIDE AND NORMAL LIPOPOLYSACCHARIDE.
-!- CATALYTIC ACTIVITY: Alpha-D-glucose 1-phosphate = alpha-D-glucose
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                 E->K: IN CTR1-4; EXHIBITS ETHYLENE-
TREATED PHENOTYPE.
D->E: IN CTR1-1; EXHIBITS ETHYLENE-
TREATED PHENOTYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A chromosomal cluster of genes encoding ADP-glucose synthetase, glycogen synthase and phosphoglucomutase in Agrobacterium
                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-UNW-2002 (Rel. 41, Last annotation update)
Phosphoglucomutase (EC 5.4.2.2) (Glucose phosphomutase) (PGM).
PGM OR EXOC OR PSCA.
Agrobacterium tumefactens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -! - SIMILARITY: BELONGS TO THE PHOSPHOHEXOSE MUTASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION.
MEDIINE-90170885; PubMed-2307661;
MEDIINE-90170885; PubMed-2307661;
Ugalde R.A.;
"Biochemical characterization of avirulent exoc mutants of
                                                                                                                                                                                                                                                                          DB 1; Length 821;
                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                             2922D3DCD0CC15BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        542 AA
                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                     BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                           Score 38;
                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95047522; PubMed-7959036;
                                                                                                                                                                                                                                              821 AA; 90306 MW;
                                                                                                                                                                                                                                                                           52.1%;
                                                                                                                                                                                                                                                                                         57.18;
                                                                                                                                                                                                                                                                                                                                                               761 AAVGFKCKRLEIPR 774
                                                                                                                                                                                                                                                                                                                                     1 SARGTKCLRKKIPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Uttaro A.D., Ugalde R.A.;
"A chromosomal cluster of
                                                                                                                                                                                                                                                                                                      8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 150:117-122(1994).
                                                                                                                141
809
565
578
676
596
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                      596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=358;
                                                                                                                                                                                                                 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-A348
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                                                                                                                                                                        ACT_SITE
MUTAGEN
                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                   MUTAGEN
                                                                                                                                                                                                                                                                                                        Matches
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Hypothetical protein; Transferase; Glycosyltransferase;
Complete proteome.
SEQUENCE 550 Aa; 64278 MW; DB8B5CCEIBA24CB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                                                                                             RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                  SOURCE STATE STATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE-96337999; PubMed-8680807;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Sutton G.G., Rikhess E.F., Weinstock K.G., Merrick J.M., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Ngnyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts R.M., Hurst M.A., Kalne B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 273:1058-1073(1996).
-1- SIMILARITY: BELONGS TO THE QUEUINE TRNA-RIBOSYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                            FORMS THE PHOSPHOSERINE INTERMEDIATE
                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                 Score 37; DB 1; Length 542;
Pred. No. 32;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus. NCBL_TaxID=2190;
                                                                                                                                                                                                                                                               BY SIMILARITY).
F40AD8ED482E905D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
5-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGRFAMs; TIGR00449; tgt_general; 1.
TIGRFAMs; TIGR00451; unchar_dom_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interPro; IPR004804; Arcsn_tRNA_tgt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002616; Que_tRNAtransf.
InterPro; IPR004521; Unchar_dom_2.
                                                   IPR001485; PG/PMM_mutase.
       AF033856; AAD03475.1; -. P00949; 3PMG.
                                                                           Pfam; PF00408; PGM_PNH; 1.
Pfam; PF02879; PGM_PNLI; 1.
Pfam; PF02879; PGM_PNM_III; 1.
Pfam; PF02880; PGM_PNM_III; 1.
                                                                                                                                                                                                                                                                                        542 AA; 57802 MW;
                                                                                                                                                                PRINTS; PR00509; PGMPMM.
PROSITE; PS00710; PGM_PMM; 1.
Isomerase; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                 50.7%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein MJ0436.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fam; PF01472; PUA; 1.
fam; PF01702; TGT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                4 GTKCLRKKIP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 GTSGLRKKVP 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR002478;
                                                                                                                                                                                                                                                                                                                                                       Local Similarity
hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MJ0436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     annaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X436_METJA
Q57878;
                                                   nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interPro;
                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                              ACT_SITE
                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y436_METJA
                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
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                                                        ö
                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Bifunctional dihydrofolate reductase-thymidylate synthase (DFR-TS)
[Includes: Dihydrofolate reductase (BC 1.5.1.3); Thymidylate synthase (BC 2.1.1.45)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIHYDROFOLATE REDUCTASE FAMILY.
-!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE THYMIDYLATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trypanosoma brucel brucel.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-96089823; PubMed-8538681;

Gamarro F., Yu P.L., Zhao J., Edman U., Greene P.J., Santi D.;

"Trypansonama brucel dihydrofolate reductase-thymidylate synthase:
"Trypansonama brucel dihydrofolate regimeration of the enzyme.";
Mol. Biochem. Parasitol. 72:11-22(1995).

-!- CATALITIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP -
dihydrofolate + dTMP.

-!- CATALITIC ACTIVITY: 5,6,7,8-tetrahydrofolate + NADP(+) - 7,8-
dihydrofolate + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Multifunctional raryms; Oxidoreductase; Transferase; NADP;
Methyltransferase; Nucleotide biosynthesis; One-carbon metabolism.
DOMAIN 1242 DIHYDROFOLATE REDUCTASE.
                                                        ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 527; 47;
  Length 550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- PATHWAY: Deoxyribonucleotide biosynthesis.
-i- SUBUNIT: HOWODIWER (BY SIMILARITY).
-i- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE
                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y SIMILARITY.
39982FC553BF7601 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THYMIDYLATE SYNTHASE
Score 37; DB 1;
Pred. No. 32;
1; Mismatches
                                                                                                                                                                                                                                                                                                                   527 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0070; DHFR.
PRINTS; PRO0108; THYMDSNTHASE.
PRODOM; PDO001180; THYMIGYJAL_SYNt; 1.
PROSITE; PS00075; DHFR; 1.
PROSITE; PS00091; THYMIDYLATE_SYNTHASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001796; DHFR.
InterPro; IPR000398; Thymidylat_synt.
Pfam; PF00186; DiHfolate_red; 1.
Pfam; PF00303; thymidylat_synt; 1.
                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                        (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58804 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U20781; AAA91362.1; -. HSSP; P13100; 1CI7.
     50.7%;
61.5%;
                                                                                                                                                                        457 SEKGAKLLWKKIP 469
                                                                                                                1 SARGTKCLRKKIP 13
                                Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        527 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=5702;
                                                                                                                                                                                                                                                                                                                DRTS_TRYBB
Q27783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
SEQUENCE
     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                           DRTS_TRYBB
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1 SARGTKCLRKKIP 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 8; Conserv
 [1]
SEQUENCE FROM N.A.
                                                                                               MEDLINE-20512590;
                                                                                                                                                                                                                     (DNA) (N)
                                                                                                                                                                                                                                                                                                                                                                                                                     REBASE; 4832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEG. outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                         *Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
  Gaps
                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 24:4420-4449(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL LIPOPROTEIN MG338 HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
DNA polymerase (EC 2.77.7) (Contains: Endonuclease PI-ThyII
(EC 3.1...) (Thy pol-1 intein); Endonuclease PI-ThyI (EC 3.1...)
                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical lipoprotein MG338 homolog precursor (P02_orf1300).
MPD488 OR MP353.
Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 N-ACYL DIGLYCERIDE (POTENTIAL).
143063 MW; B8236A003A9879DB CRC64;
                                                                                                                                                                                                                                                                                                                   (Potential).
-!- SIMILARITY: BELONGS TO THE MG307 / MG309 / MG338 FAMILY.
                                                                                                                                                                                                                                                    Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Hypothetical protein; Lipoprotein; Membrane; Signal;
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 1; 1
Pred. No. 1.1e+02;
3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1668 AA.
                                                                                             PRT; 1300 AA.
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; Pubmed-8948633;
 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EC 3.1. -. -) (Thy pol-1 intein (Thy pol-2 intein)] (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE000033; AAB96001.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermococcus hydrothermalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |::||| :|| |
1251 SSQGTKTIRKPKP 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SARGTKCLRKKIP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
7; Conservative
                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26
1300
                      5 TKCLRKKIP 13
                                           TRILRKKIP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1300 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=46539;
                                                                                                                                                                                               NCBI_TaxID-2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DPOL_ТНЕНҮ
О9ИН05;
                                                                                              Y338_MYCPN
P75296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
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                                                                                                                                                                                                                             Querellou J.J.E., Cambon M.A., Lesongeur F.O., Barbler G.;
"Thermococcales taxonomy and phylogeny based on the comparative use of
16S rDNA, 16S-23S rDNA intergenic spacer and family B DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PTM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES A POST-TRANSLATIONAL EXCISION OF THE INTERVENING REGION (INTEIN) FOLLOWED BY PEPTIDE LIGATION (Potential).
-!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
-!- SIMILARITY: IN THE INTEIN SECTION; BELONGS TO THE HOWING ENDONUCLEASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PSO0116; DNA_POLYMERASE_B; FALSE_NEG.
PROSITE; PS50818; INTEIN_C_TER; 2.
PROSITE; PS50819; INTEIN_ENDONUCLEASE; 2.
PROSITE; PS50817; INTEIN_N_TER; 2.
Transferase; DNA-directed DNA polymerase; DNA replication;
DNA-binding; Hydrolase; Nuclease; Exonuclease; Multifunctional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein splicing; Autocatalytic cleavage; Endonuclease; Intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENDONUCLEASE PI-THYI (POTENTIAL).
DNA POLYMERASE, 2ND PART.
ENDONUCLEASE PI-THYII (POTENTIAL).
DNA POLYMERASE, 3RD PART.
W; 5EEBB05EFEDA71C8 CRC64;
                                                                                                                   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA POLYMERASE, 1ST PART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR002064; DNA_pol_B.
Interpro; IPR003586; Hedgehog_hintC.
Interpro; IPR0023587; Hedgehog_hintN.
Interpro; IPR004023; Intein.
Interpro; IPR004042; Intein.
Interpro; IPR00404578; Pol2.
Pfam; PP00136; DNA_pol_B; I.
Pfam; PP03104; DNA_pol_B=exo; I.
                                                                                                                                                                                                           PubMed-11058140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00106; DNAPOLB.
PRINTS; PR00379; INTEIN.
SNART; SN00305; HintC; 2.
SNART; SN00306; HintN; 2.
SNART; SN00486; POLBC; 1.
TIGRFAMS; TIGR00592; pol2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ245819; CAC18555.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193319
                                                                                                                                                                                   CHARACTERIZATION OF PI-THYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          995
1044
1433
1668
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1045 143
1434 166
1668 AA;
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Gaps

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Length 1668;

Score 36; DB 1; Length 166
Pred. No. 1.4e+02;
Mismatches 4; Indels

49.3%;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                         *Acrogranin, an acrosomal cysteine-rich glycoprotein, is the precursor of the growth-modulating peptides, granulins, and epithelins, and is expressed in somatic as well as make germ cells."; wol. Reprod. Dev. 34.233-243(1993).
--- FUNCTION: GRANULINS HAVE POSSIBLE CYTOKINE-LIKE ACTIVITY. THEY MAY PLAY A ROLE IN INFLAMMATION, WOUND REPAIR, AND TISSUE REMODELING.
                                                                                                                                                                  01-DEC-1992 (Rel. 24, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Granulins precursor (Acrogranin) (Contains: Granulin 1; Granulin 2;
Granulin 3; Granulin 4; Granulin 5; Granulin 6;
                                                                                                                                                                                                                                                                        Cavia porcellus (Guinea pig).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;

Mammalia; Butheria; Rodentia; Hystricognathi; Caviidae; Cavia.

NCBL_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRANULIN 5.
GRANULIN 6.
GRANULIN 7.
N-LINKED (GLCNAC. ...) (POTENTIAL).
EE7C9FC8F21CB8A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-93228994; PubMed-8471244;
Baba T., Hoff H.B. III, Nemoto H., Lee H., Orth J., Arai Y.,
                                                                                                           591 AA.
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 4-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 - PTM: GRANULINS ARE DISULFIDE BRIDGED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACROGRANIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRANULIN 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRANULIN GRANULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRANULIN
                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fam; PF00396; granulin; 7.
MART; SM00277; GRAN; 6.
PROSITE; PS00799; GRANULINS; 6.
                                                                                                                                                 01-DEC-1992 (Rel. 24, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [PR000118; Granulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62586 MW;
ZMBL; M86735; AAA37030.1;
                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                    ISSUE-Testis;
                                                                                                                                                                                                                                               Fragment).
                                                                      RESULT 15
GRN_CAVPO
ID GRN_CAVPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytokine;
NON_TER
SIGNAL
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SEQUENCE
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Query Match 48.6%; Score 35.5; DB 1; Length 591;
Best Local Similarity 35.0%; Pred. No. 65;
Matches 7; Conservative 5; Mismatches 1; Indels 7; Gaps
2 ARGIKCLRKK-----IPR 14

ä

564 SQGTRCVHKKSLLHWDSLPR 583

9 9 Search completed: July 8, 2003, 16:25:03 Job time: 8.82051 secs

OM protein - protein search, using sw model

July 8, 2003, 16:17:10; Search time 30.1538 Seconds (without alignments) 95.665 Million cell updates/sec Run on:

US-09-824-647-5 73 1 SARGTKCLRKKIPR 14

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 segs, 206047115 residues Searched:

. 671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:* sp_invertebrate:*
sp_mammal:* sp_organelle:* sp_archea:* sp_bacteria:* sp_plant:* sp_rodent:* sp_virus:* SPTREMBL_21:* sp_fungi:* sp_human:* sp_phage: * sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

SUMMARIES

Description	O9d2v3 mus musculu	09h8s1 homo sapien	Q58811 methanococc	Q8qn63 ectocarpus	Q9dcp5 mus musculu	Q9qxt5 mus musculu	Q9jk23 mus musculu	O8vuf4 azoarcus ev	O8zdd9 yersinia pe	08sv43 encephalito	Q9daq5 mus musculu	Q9y3k4 homo sapien	Q8wld8 acridocarpu	Q22385 caenorhabdi	Q91zk0 mus musculu	Ogc789 arabidonais
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er G	09D2V3	9H8S1	058811	080N63	Q9DCP5	090хт5	Q9JK23	8VUF4	98ZDD9	.08SV43	09DAG5	9Y3K4	8WLD8	22385	Q912K0	090789
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% Query Match Length DB	589	413	452	202	265	278	289	355	555	124	247	252	254	288	452	777
% Query Match	93.2	79.5	56.2	54.8	54.8	54.8	54.8	54.8	54.8	53.4	53.4	53.4	53.4	53.4	53.4	53.4
Score	89	28	41	40	40	40	40	40	40	. 39	39	39	39	39	. 39	36
Result No.	1	7	m	4	5	9	7	σ ο	Ø	10	11	12	13	14	15	16

~~ 0~~~		Q8wla3 mezia arauj Q8wl88 lasiocarpus Q8wlb4 ryssopterys Q8wlc7 peregrina l Q8wlc7 peregrina l		OBWLC3 janusia cal OBWLD8 peirocha gl OBWLD3 sphedamnoca OBWLD3 heteroptery	
		•			
				•	
P74081 Q9W3W0 Q91FT0 Q8RXS1	08WL97 08WL93 08WL92 08WLB5 08WLD6	08WLA3 08WL88 08WLB4 08WLC7	28WL76 28WL24 28WLD1 28WL72 28WL72	28WLC3 28WLB8 28WLB3 28WLA5	DBWL90 DBWL87 DBWL86 DBWL86
2012		 		6	
942 1123 99 175	190 207 213 223 228	2222 2222 2244 2444 244	246 246 246 246	247 247 247	248 248 248 249
53.4 52.1 52.1 52.1	52.1 52.1 52.1 52.1	52.1 52.1 52.1 52.1	522.1 522.1 522.1 582.1 582.1	52.1 52.1 52.1	52.1 52.1 52.1 52.1 52.1
		8 8 8 8 8 8 8 8 8 8 8 8		88888	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
17 18 20 21	22 23 25 26	27 28 30	3 3 4 3 5 5 6 5 5 4 3 5 5	37 38 39 40	4 4 4 4 4 4 5 4 5 4 5 4 5 4 5 4 5 4 5 4

ALIGNMENTS

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6 KCLRKKIP 13
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-ESV-1;
                                                                                                                                                                                                  IGR; MJ1416;
                                                                                                                                                                                                                                             Hypothetical
SEQUENCE 4:
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                                                                                                                                                                                                                                                                                                                                                                                                               080N63;
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Q9DCP5;
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                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                TISSUB-OVARIAN CARCINOMA;
ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sato H., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugamara M.
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watamabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Ninomiya K., Iwayanagi T.,
Ninomiya K., Iwayanagi T.,
                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                  Length 589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 58; DB 4; Length 413;
Pred. No. 0.0042;
3; Mismatches 1; Indels
                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            "NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK023348; BAB14535.1; -.
                                                  PROSITE; PS00799; GRANULINS; 7.
PROSITE; PS00118; PA2_HIS; UNKNOWN_1.
SEQUENCE 589 AA; 63405 MW; 1DE8229C413CA292 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00799; GRANDINS; UNKNOWN 4.
PROSITE; PS00118; PA2_HIS; UNKNOWN 1.
SEQUENCE 413 AA; 44132 MW; 0E3767A44BE314EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MJ1416.
Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococci; Methanococcales;
                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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                                                                                              93.2%; Score 68; DB 11;
100.0%; Pred. No. 6.2e-05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                       413 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000118; Granulin.
InterPro; IPR001211; PhospholipaseA2.
        InterPro; IPR000118; Granulin.
InterPro; IPR001211; PhospholipaseA2.
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                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanococcaceae; Methanococcus
                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-70N-2002 (TrEMBLrel. 21, 03-ARL) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 06, (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00396; granulin; 4.
SMART; SM00277; GRAN; 4.
                               Pfam; PF00396; granulin; 7. SMART; SM00277; GRAN; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2002 (TrEMBLrel. 20, Hypothetical protein MJ1416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SARGTKCLRKKIPR 14
                                                                                        Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 71.4
Watches 10; Conservative
                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-9606;
MGI:95832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 058811;
01-JUN-1998
                                                                                                                                                                                                                      09H8S1
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Q58811
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Delaroque N., Bothe G., Pohl T., Knippers R., Mueller D.G., Boland W., "The complete nucleotide sequence of the Ectocarpus siliculosus virus
MEDLINE-96337999; PubMed-8688087;
MEDLINE-96337999; PubMed-8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reigh C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Gåodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                          Science 273:1058-1073(1996).
-!-SMILLARITY: STRONG, TO M.THERMOAUTOTROPHICUM MTH1525, A.FULGIDUS
---BAZ363 AND F.SCIEATARICUS ORF C04046.
EMBL, U67582, AAB94246.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ectocarpus siliculosus virus.
Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phaeovirus.
NCBI_TaxID-37665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 12; Length 205; Pred. No. 7.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF204951; AAK14640.1; -.
SEQUENCE 205 AA; 24317 MW; C3A21D3650D46F32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Vascular endothelial zinc finger 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000728; AIRS_related
Pfam; PF00586; AIRS; 1.
Pfam; PF02769; AIRS_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.8%;
66.7%;
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87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 87.5.
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Strausberg R.
                                                             'ISSUE-LIVER;
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                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9JK23;
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ID 08
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DT 01
DE 6-
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                                                                                                              Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishli Y., Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishli Y., Arakawa T., Hara A., Fukunishi Y., Kiyosawa H., Kodoca S., Yamanaka I., Saito T., Okazaki Y., Golobori T., Bono H., Rasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Releischmann W., Gassterland T., Gissi C., King B., Kochiwa H., Rachill P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Ra Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Rasaki R., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Rabincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                          *Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
EMBL; AK002601; BAB22222.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus homolog of HLA class III region containing NOTCH4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 11; Length 265;
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TIEMBLIE). 13, Created)
01-MAY-2000 (TIEMBLIE). 13, Last sequence update)
01-JUN-2002 (TIEMBLIE). 21, Last annotation update)
NOTCHG-like protein (Vascular endothelial zinc finger 1).
VEZF1 OR ZNEU1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00022; EGF_1; UNRNOWN_1.
PROSITE; PS01186; EGF_2; UNRNOWN_1.
PROSITE; PS01187; EGF_CA; 1.
SEQUENCE 265 AA; 28665 MW; D81EC3DA884FF97E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    278 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                        STRAIN-C57BL/6J; TISSUE-KIDNEY;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1313291; Vezfl...
InterPro; IPR000561; EGF-11ke...
InterPro; IPR001881; EGF_Ca...
Pfam; PF00008; EGF; 2...
SMART; SM00181; EGF, 2...
SMART; SM00001; EGF_L1ke; 2...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 SADGTRCLSKEGP 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                               Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                            SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9QXT5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene.
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDIJNE-20329221; PubMed-10872820;
Vidal-Taboada J.M., Lu A., Pique M., Pons G., Gil J., Oliva R.;
"Down syndrome critical region gene 2: expression during mouse development and in human cell lines indicates a function related to cell proliferation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                  MGD; MGI:1343-91; Vezfl.

MGD; MGI:1343-91; Vezfl.

InterPro; IPR000561; EGF-11ke.

InterPro; IPR00081; EGF_2.

SMART; SM00001; EGF_1.

SMART; SM00001; EGF_1.

PROSITE; PS00186; EGF_2.

PROSITE; PS01186; EGF_2; UNRNOWN_1.

PROSITE; PS01186; EGF_2; UNRNOWN_1.

PROSITE; PS01187; EGF_CA; II.

Calcium-binding; EGF-11ke domain; Glycoprotein; Repeat.

SEQUENCE 278 AA; 30125 MW; 863159F567102PA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                               Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AF184973; AAF01322.1; --
EMBL; BC024610; AAH24610.1; --
HSSP; P00740; 1EDM.
Martinez T., Hoffman R., O'Hara P.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289 AA; 33104 MW; FEB4F7FDDC020F06 CRC64;
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01-MAR-2002 (TIEMBLE-1. 20, Created)
01-MAR-2002 (TIEMBLE-1. 20, Last sequence update)
01-JUN-2002 (TIEMBLE-1. 21, Last annotation update)
6-hydroxycyclohex-1-ene-1-carboxyl-CoA dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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EMBL; AJ238270; CAB87195.1; -.
MGD; MGI:1860263; Dscr2.
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Pred. No. 11;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 AA.
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Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 10;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last seq
01-DEC-2001 (TEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.8%;
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256 SSRSLKCLVKNIP 268
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Matches 8; Conservative
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DSCR2 OR MC21-LRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                    SEQUENCE FROM N.A.
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124 AA.

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Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H.,
Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackembush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Iyons P., Marchionii L., Mashima J., Maszarelli J., Monbaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sassaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.
Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Rohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence and gene compaction of the eukaryote parasite Encephalitozoon cuniculi.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21576510; PubMed-11719806; MEDLINE-21576510; PubMed-11719806; Metanika M.D., Duprat S., Cornillot E., Metanika G., Thomarat F Prensier G., Barbe V., Peyretaillade E., Brottler P., Wincker Belbac F., El Alaoul H., Peyret P., Saurin W., Gouy M., Weissenbach J., Vivares C.P.;
                                                                                                                                                                                                                                          Eukaryota; 'Microsporidia; Unikaryonidae; Encephalitozoon.
NCBL_raxID=6035;
                                                                                                                                                                                                                                                                                                                                                                                                             Genoscope; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 414:450-453(2001).
EMBL. AL590447. CAD2556.1; -.
Hypothetical protein.
SEQUENCE 124 AA; 13235 MW; CBE8854640A8D841 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                           Last sequence update)
Last annotation update)
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PRT;
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MEDLINE-21085660; PubMed-11217851;
                                                             01-JUN-2002 (TrEMBLrel. 21, Crea 01-JUN-2002 (TrEMBLrel. 21, Last 01-JUN-2002 (TrEMBLrel. 21, Last Hypothetical protein ECUO7_0240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -JUN-2001 (TrEMBLrel. 17,
-JUN-2001 (TrEMBLrel. 17,
-JUN-2001 (TrEMBLrel. 17,
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Encephalitozoon cuniculi.
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   PRELIMINARY;
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Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                STRAIN-GB-MI
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      ID ACCOORDING TO A STANDARD ACCOORDING THE ACCOUNTY ACCOUNTY
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"Genome sequence of Yersinia pestis, the causative agent of plague."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-21470413; Pubmed-11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M. Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamin N., Bolroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                 Bacteria; Proteobacteria; beta subdivision; Rhodocyclus group;
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Pred. No. 20;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40; DB 2; Length 355;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                     Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AJ428529; CAD21637.1; -.
                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002085; Adh_zn_family.
InterPro; IPR00345; CytC_heme_bind.
Pfam: PF00107; adh_zinc; 1.
PROSTIE: PS00190; CYTCCHROME_C; UNKNOWN_1.
SEQUENCE 355 AA; 38211 MW; 5E1D930131F800A6 CRC64;
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PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
Aminoacyl-trNA synthetase; Ligase; Complete proteome.
SEQUENCE 555 AA; 63750 MW; AD3C68D6FB56C0B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Glutaminyl-tRNA synthetase (EC 6.1.1.18).
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InterPro; IPR000924; Glu_tRNA-synt_lc.
InterPro; IPR001412; tRNA-synt_l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                          Mohr K., Herrmann H., Burchhardt G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.8%;
72.7%;
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TGRGNRCLSQKMP 111
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Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                           NCBI_TaxID=59406;
                                       Azoarcus evansii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yersinia pestis
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                                                                                                                                                                                                                          STRAIN-KB740;
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01-MAR-2002 01-MAR-2002

RESULT 10

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Q8ZDD9

Matches

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Gaps

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Length 124;

5,

247 AA

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J. Biol. Chem. 0:0-0(2001).
EMBL; AF421891; AAL16940.1;
InterPro; IPR004979; TF_AP2.
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                                                                                 3 RGTKCLRKKIP 13
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                                                Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                            T11A5.5 protein.
                                                                                                                                                                                                                                                             NCBI_TaxID=6239;
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                   SEQUENCE
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Q22385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Malpighiaceae; Acridocarpus.
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Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
          "Functional annotation of a full-length mouse cDNA collection.";
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                                                                        Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 4; Length 252;
Pred. No. 15;
3; Mismatches 4; Indels
                                                                                             3; Indels
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Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL031224; CAB41306.1; -.
InterPro; IPR004979; TF_AP2.
Pfam; PF03299; TF_AP-2; 1.
                   Nature 409:685-690(2001).
EMBL, AKO05861; BABA2B1.1; -
MGD; MGI:192717; 1700011E24Rik
SEQUENCE 247 AA; 27631 MW; 5A9BBD78EE7BD9FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 252 AA; 27527 MW; 461BB71DC17C5980 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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Last annotation update)
                                                                       DB 11;
15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254 AA.
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                                                                       53.4%; Score 39; DB 60.0%; Pred. No. 15; tive 1; Mismatches
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EMBL; AF351016; AAL35030.1; -.
InterPro; IPR002128; Oxidored_q1_C.
Pfam; PF01010; oxidored_q1_C; 1.
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50.0%;
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SKNGGRCLREKLDR 71
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Best Local Similarity 50.v.
                                                                       Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
 Hayashizaki Y.;
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Q8WLD8
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Rhabditidae; Peloderinae; Caenorhabditis.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                       Length 254;
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Pred. No. 17;
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z72515; CA96685.1; -.
INLECPRO; IRR000896; Hemocyanin.
PROSITE; PS0010; HEMOCYANIN_2; UNKNOWN.1.
PROGUNCE 288 AA; 32287 MW; EBIEEAOEF945F9BD CRC64;
                                           EESD5E653867D926 CRC64;
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Last annotation update)
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Pred. No. 15;
3; Mismatches
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MEDLINE-99069613; PubMed-9851916;
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254 254
254 AA; 29522 MW;
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01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 70.0
Matches 7; Conservative
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DR Pfam; PF03299; TF_AP-2; 1. SQ SEQUENCE 452 AA; 49547 MW; 6722342B15CDF9EB CRC64; Ouery Match. 53.4%; Score 39; DB 11; Length 452;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps

장 임 Search completed: July 8, 2003, 16:28:00 Job time: 32.1538 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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July 8, 2003, 16:08:55; Search time 47.5 Seconds (without alignments) 53.300 Million cell updates/sec protein search, using sw model OM protein Run on:

US-09-824-647-6 Perfect score: Title:

1 EKAPAHLSLPDPQALKRDV 19 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 seqs, 133250620 residues Searched:

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT: /gcgdata/geneseq/geneseqp-embl/AA1980.DAT /geneseqp-embl/AA1993 /gcgdata/geneseg/genesegp-embl/AA1988 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA19 SIDS2/gcgdata/geneseq/genesegp-emb1/AA19 /gcgdata/geneseq/genesedp-emb1/AA19 /SIDS2/gcgdata/geneseg/genesegp /SIDS2/gcgdata/geneseg/ A_Geneseq_101002:4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Human GP88 autocr1	Human protein sequ	Human epithelin pr	Granulin sequence.	Human GP88 autocr1	Human granulin/epi	Human cancer assoc	Rat epithelin prec	Bovine epithelin p	Mouse GP88 autocri
	Ð	AAW85480	AAB94550	AAR14326	AAR48673	AAW85475	AAE20521	AAB43971	AAR14325		
		20	22	12	14.	20	23	21	12	12	20
	Query Match Length DB	:							589		
ø	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	64.3	54.1	51.0
	Score	86	96	96	96	98	96	98	63	53	20
	Result No.		7	æ	4	5	9	7	æ	6	10

-	Novel human diagno	Human protein sequ	Human polypeptide	Human protein segu	Human protein SEQ	Human polypeptide	Human protein SEQ	Propionibacterium		Peptide #1537 enco	Protein #1474 enco	Human brain expres	Human bone marrow		Peptide #1524 enco	Peptide #1458 enco	Human peptide enco	Mouse GP88 autocri	A. thallana MYB26	Mouse epithelin pr	Pseudomonas aerugi	Human immune/haema	Propionibacterium	Human secreted pro	nervou	Novel human diagno	Herpesvirus entry	nectin		ovarie	_	Novel human diagno	Human ORF706 prote	Human haematologic	
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AAE20520	ABG28448	AAB94335	AAM3967	AAB9297	AAM8027	AAM41460	AAM79295	AAU56854	ABB28848	ABB34031	ABB1947	AAM54803	AAM67188	AAM15045	AAM27487	AAM0277	ABG36851	AAW8547	AAM4974	AAR14327	AAU33715	AAM82920	AAU51132	AAG02780	ABB16381	ABG04056	AAY32389	AAE23296	ABG18843	ABP41837	ABG28883	ABG08403	ABP3173	AAM8191	
23	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	23	20	23	12	22	22	22	21	22	22	21	23	22	23	22	22	23	22	
589	730	324	828	828	829	829	996	55	. 59	29	29	29	29	29	. 59	59	29	13	367	589	619	22	62	114	117	245	479.	479	487	522	812	820	110	99	
51.0	50.0	48.0	48.0	48.0	48.0	48.0	48.0	45.9	45.9	45.9	45.9	45.9	45.9	45.9		45.9	45.9	44.9	44.9	44.9	44.4	43.9	43.9	43.9	43.9	43.9	43.9	43.9	43.9	43.9	43.9	43.9	43.4	42.9	
20	49	47	47	47	47	47.	47	45	45	45	45	45	45	45	45	45	45	44	44	44	43.5	43	43	43	43	43	43	43	43	43	43	.43	42.5	42	
11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	. 45	

ALIGNMENTS

RESULT 1 AAW85480

GP88; granulin; epithilin; human; growth factor; autocrine; tumour; cancer; viral infection; antagonist; therapy; diagnosis; antigen; Human GP88 autocrine growth factor antigenic peptide E19V. AAW85480 standard; Peptide; 19 AA. 15-MAR-1999 (first entry) Homo sapiens. antibody. AAW85480;

W09852607-A1.

98WO-US10555. 22-MAY-1998; 26-NOV-1998.

970S-0991862. 970S-0863079. 16-DEC-1997; 23-MAY-1997;

(SERR/) SERRERO G.

Serrero G;

WPI; 1999-045276/04.

Composition containing antagonist of growth factor GP88 - useful for treating cancer and viral diseases and also for diagnosing disease

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Human epithelin precursor.
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                                                                                                                                                                                                                                                                                                 Local Similarity
nes 19; Conserv
                                                                                                                                                                                                                                                          413 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                 This is the amino acid sequence of peptide E19V, comprising amino acid residues E340-V364 of human GP88 (see AAW85475). GP88 is an EAB alycoprotein autocrine growth factor that is expressed in a tightly regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which acts as a stringently required growth stimulator for the tumorigenic cells. E19V was used to raise neutralising antibodies to GP88. Antagonists to GP88, such as anti-GP88 antibodies, are used to treat diseases associated with increased expression of GP88, particularly cancer but also viral infections. Anti-GP88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamamoto J;
                                                                                                                                                                                                   antibodies can also be used as diagnostic reagents and to deliver toxins or other compounds to GP88-expressing cells.
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                                                                                                                                                                                                                                                                       100.0%; Score 98; DB 20; Length 19; 100.0%; Pred. No. 1.3e-07;
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Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                   0; Mismatches
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                            Example 8; Page 45; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                1 EKAPAHLSLPDPQALKRDV 19
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11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0133767.
09-JUN-2000; 2000JP-0241899.
from altered GP88 expression
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Matches 19; Conservative
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Ishii S,
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oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide comprises a 3'-end sequence, where the polynucleotide which comprises a 3'-end sequence, where the polynucleotide comprises a 1'-end sequence, where the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense#therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length coMAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length coMAs. The primers allow obtaining of the full-length compass. The primers allow obtaining of the full-length compassing the primers allow obtaining and the full-length compassing the primers allow obtaining of the full-length compassing the primers allow obtaining and the full-length compassing the primers allow obtaining and the full-length compassing the primers allow obtaining and the full-length compassing the primers allow obtaining allow the full-length compassing the full-length compassi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonuclectides, all of which are used in the exemplification of the present investion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 413;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 98; - DB 22;
100.0%; Pred. No. 3.7e-06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ET; growth regulation; inhibition; stimulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "claim 3, page 53"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "claim 4, page 53"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               page 53'
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| 1..593
| /label= precursor
| ...te= "claim 1, pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR14326 standard; Protein; 593 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= EP .//note= "claim 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EKAPAHLSLPDPQALKRDV 19
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/note- "claim
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/note= "claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "claim
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/label= EP-1
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Gaps

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Composition containing antagonist of growth factor GPB8 - useful for treating cancer and viral diseases and also for diagnosing disease from altered GPB8 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is the amino acid sequence of human GP88, an 88 kDa glycoprotein autocrine growth factor and epithilin/granulin precursor that is expressed in a tightly regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which acts as a stringently required growth stimulator for the tumorigenic cells. Inhibition of GP88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GP88; granulin; epithilin; human; growth factor; autocrine; tumour; cancer; viral infection; antagonist; therapy; dlagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression or action in the tumorigenic cells results in an inhibition of the tumorigenic properties of the overproducing cells. Antagonists to GPBB are used to treat diseases associated with increased expression of GPBB, particularly cancer but also viral infections. Fragments of GPBB are used to raise specific
                                                                                 The granulin inhibits keratinocytes and is useful in formulations for promoting the healing of wounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
340..364
/note= "E19V peptide used to raise antibody"
/note= "A14R peptide used to raise antibody"
New cystine rich granulin peptide(s) from leucocyte(s) - are keratinocyte inhibitors useful topically for wound healing
                                                                                                                                                                       Length 593;
                                                                                                                                                                                                       Indels
                                                                                                                                                                     Score 98; DB 14;
Pred. No. 5.5e-06;
                                                                                                                                                                                                       Mismatches
                                                   Oisclosure; Figure 4c; 53pp; English
                                                                                                                                                                                                                                                                                                                                                              AAW85475 standard; Protein; 593 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human GP88 autocrine growth factor.
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                                                                                                                                                                                                                                                          346 EKAPAHLSLPDPQALKRDV 364
                                                                                                                                                                                                                                         1 EKAPAHLSLPDPQALKRDV 19
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                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US10555
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                                                                                                                                                     Query Match
Best Local Similarity 100.v.,
                                                                                                                                                                                                                                                                                                                                                                                                                                  15-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-045276/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SERR/) SERRERO G.
                                                                                                                                        593 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAV82825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9852607-A1
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23-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serrero G;
                                                                                                                                                                                                                                                                                                                                                                                                 AAW85475;
                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                              RESULT 5
AAW85475
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                                                                                                                                                                                                                                                                                                         ET-1 is a bifunctional growth regulator, capable of stimulating the growth of some cell types while inhibiting the growth of others. ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory bloactivity. In contrast, however, ET-2 is apparently not capable of eallotling the growth stimulatory activity characteristic of ET-1 and, in fact, antagonises this ET-1 activity. See also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                        New cysteine-rich growth modulating proteins, epithelins - useful as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Granulin; keratinocytes; wound healing; inhibition; peptide; granulocytes; leucocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 98; DB 12;
Pred. No. 5.5e-06;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Valine encoded by ATG."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Glycine encoded by CAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR48673 standard; Protein; 593 AA
                                                                                                                                                                                                                                                                            Disclosure; Fig 22; 97pp; English.
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                                   910S-0083796.
                                                                                     (BRIM ) BRISTOL-MYERS SQUIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
nes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                       Plowman GD;
                                                                                                                                                       WPI; 1991-325168/44.
N-PSDB; AAQ14339.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   593 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Granulin sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAQ49052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens:
                                   13-MAR-1991;
03-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09315195-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35-AUG-1993
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                                                                                                                     Shoyab M,
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AAR48673;

Sequence

Query Match

Best Loc Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           granulin precursor; GP88; cytostatic; tumoùrigenicity; tamoxifen; pplastic; antioestrogen therapy; skin cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing tumorigenicity in a human, comprising obtaining a cell sample, detecting GP88 in the cells, and determining the number of GP88 positive cells in the sample -
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Region used as antigen to develop anti-human GP88 neutralising antibody"
antibodies (used as antagonists, as diagnostic reagents and for delivering toxins or other compounds to GPBB-expressing cells) and to screen for antibodies. Methods are provided for diagnosing disease, or determining susceptibility to disease, resulting from altered GPBB activity.
                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                           Length 593;
                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human granulin/epithelin precursor (GP88) protein.
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                                                                                                                                                                                                                        100.0%; Score 98; DB 20; 100.0%; Pred. No. 5.5e-06;
                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Encoded by AAG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE20521 standard; Protein; 593 AA.
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                                                                                                                                                                                                                                                                                                                                                                FKAPAHLSLPDPQALKRDV 364
                                                                                                                                                                                                                                                                                                                                      1 EKAPAHLSLPDPQALKRDV 19
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                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    346..364
                                                                                                                                                                                              WPI; 2002-267529/31.
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                                                                                                                                                                  593 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAD32850.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antineoplastic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAY-1997;
08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Serrero G;
                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                          346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE20521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human;
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ID AAI
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sample contains less than 10 % GP08, or less than 5 % GP08 positive cells. The present sequence is human granulin/epithelin precursor (GP08)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dermatological; neuroprotective; thrombolytic; coaquiant; noctropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer -
                                                                                     Length 593,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer associated gene; cancer antigen; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cancer associated protein sequence SEQ ID NO:1416.
                                                                                                                    100.0%; Score 98; DB 23; 100.0%; Pred. No. 5.5e-06;
                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 2094-2096; 2352pp; English.
                                                                                                                                                                                                                                                                                                                                     AAB43971 standard; Protein; 621 AA.
                                                                                                                                                                                                                     EKAPAHLSLPDPQALKRDV 364
                                                                                                                                                                                                 1 EKAPAHLSLPDPQALKRDV 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAR-2000; 2000WO-US05882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0124270.
                                                                                                                                                                                                                                                                                                                                                                                                                08-FEB-2001 (first entry)
                                                                                                                                        Local Similarity 100.
nes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-587533/55.
N-PSDB; AAC78180.
                                                                                 593 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40200055350-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                              AAB43971;
                                                                                 Sequence
                                                                                                                      Query Match
                                            protein.
                                                                                                                                            Best Loca
Matches
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rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial.or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of
                                                                                                     Gaps
                                                                                                    ö
                                                                                  Length 621;
                                                                                                    Indels
                                                                                 DB 21;
5.8e-06;
                                                                                                                                                                                                                                                               ET; growth regulation; inhibition; stimulation.
                                                                                 Score 98; DB
Pred. No. 5.86;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            page 54"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= EP·
/note= "claim 16, page 54"
                                                                                                                                                                                                                                                                                                                                                           page 54°
                                                                                                                                                                                                                                                                                                                                                                                      "claim 13, page 54"
                                                                                                                                                                                                                                                                                                                                                                                                                 "claim 14, page 54"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "claim 17, page 54"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note- "claim 18, page 55"
                                                                                                                                                                                                                                                                                                                               "claim 11, page 54"
                                                                                                                                                                                                                                                                                                   .ocation/Qualifiers
                                                                                                                                                                                     AAR14325 standard; Protein; 589 AA
                                                                                                                                                                                                                                                                                                                                                           "claim 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                           "claim 15,
                                                                                                                                                                                                                                                                                                             ..589
'label= precursor
                                                                                                                     Query Match 100.0%; So
Best Local Similarity 100.0%; Po
Matches 19; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                  label= EP-1
                                                                                                                                                                                                                                                                                                                                                                             'label- EP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91US-0083796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BRIM.) BRISTOL-MYERS SQUIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91WO-US02321
                                                                                                                                                                                                                                                                                                                                        .335
                                                                                                                                                                                                                                             Rat epithelin precursor
                                               the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shoyab M, Plowman GD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1991-325168/44.
N-PSDB; AAQ14338.
                                                                621 AA
                                                                                                                                                                                                                                                                                   Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-1991;
03-APR-1990;
                                                                                                                                                                                                                          17-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9115510-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-0CT-1991
                                                                                                                                                                                                         AAR14325;
                                                                  Sequence
                                                                                                                                                                                                                                                                                                     Key
Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
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                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                               Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                    RESULT 8
                                                                                                                                                                              AAR14325
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The epithelins appear to comprise several distinct members sharing significant structural homology. Two members of the epithelin family, BP-1 and EP-2, have been purified from natural sources, and cDNAs encoding these and several other members of the epithelin family have been isolated from rat (AAQ14338), human (AAQ14339), bovine, murine (AAQ14340) and chicken (AAQ14353).
ET-1 is a bifunctional growth regulator, capable of stimulating the growth of some cell types while inhibiting the growth of others. ET-2 is functionally similar to ET-1 w.r.t. growth inhibitors bloactivity. In contrast, however, ET-2 is apparently not capable of eliciting the growth stimulatory activity characteristic of ET-1 and,
                                                                                                           ET-1 is a bifunctional growth regulator, capable of stimulating the growth of some cell types while inhibiting the growth of others. ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory bioactivity. In contrast, whover, ET-2 is apparently not capable of eliciting the growth stimulatory activity characteristic of ET-1 and, in fact, antagonises this ET-1 activity. See also ARQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20.
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New cysteine-rich growth modulating proteins, epithelins - useful as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis
        New cysteine-rich growth modulating proteins, epithelins - useful as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis
                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                Score 63; DB 12; Length 589;
Pred. No. 0.65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ET; growth regulation; inhibition; stimulation.
                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                              -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovine epithelin precursor (partial).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR15426 standard; Protein; 179 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 24; 97pp; English.
                                                                               Disclosure; Fig 18; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                      :| | || || || || || || || || || || 344 KKVTASLSLPDPQILKNDV 362
                                                                                                                                                                                                                                                                                                                                                    1 EKAPAHLSLPDPQALKRDV 19
                                                                                                                                                                                                                                                                                  64.3%;
68.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91WO-0S02321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JAN-1992 (first entry)
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 68.4%
Watches 13; Cpnservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shoyab M, Plowman GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1991-325168/44.
N-PSDB; AAQ14952.
                                                                                                                                                                                                                                                  589 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9115510-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-0CT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus.
                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR15426;
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
AAR15426
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was obtained from the highly

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Indels

DB 7

Score 50; DB 2 Pred. No. 50; 1; Mismatches

51.0%; 61.1%;

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cells. Murine GP88 cDNA (see AAV82824) was obtained from the highly tumorigenic PC cell line. Antagonists to GP88 are used to treat diseases associated with increased expression of GP88, particularly cancer but also viral infections. Fragments of GP88 are used to raise specific antibodies (used as antagonists, as diagnostic reagents and for delivering toxins or other compounds to GP88 expressing cells) and to screen for antibodies. Methods are provided for diagnosing disease, or determining susceptibility to disease, resulting from altered GP88 activity
                                                                                                                                                                                                      Query Match : 51.0° Best Local Simflarity 61.1 Matches 11; Conservative
                                                                                                                                                                      589 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAY-1997;
08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-2002
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                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               AAE20520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
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     8888888888
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                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition containing antagonist of growth factor GPB8 - useful for treating cancer and viral diseases and also for diagnosing disease from altered GPB8 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the amino acid sequence of murine GPBB, an 88 kDa glycoprotein autocrine growth factor and epithilin/granulin precursor that is expressed in a tightly regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which acts as a stringently required growth stimulator for the tumorigenic cells. Inhibition of GPBB expression or action in the tumorigenic cells results in an inhibition of the tumorigenic properties of the overproducing
                                                                                                                                                                                                                                                                                                                                                                                                          GP88; granulin; epithilin; mouse; growth factor; autocrine; tumour; cancer; viral infection; antagonist; therapy; diagnosis.
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in fact, antagonises this ET-1 activity.
See also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "K19T peptide, used to raise antibody"
562..575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "S14R peptide, used to raise antibody"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "P12T peptide used to raise antibody"
                                                                                                                       4; Indels
                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note- "encoded by CTG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "encoded by TGA"
                                                                                    Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note- "encoded by AGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         Mouse GP88 autocrine growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 5; Fig 8A-D; 86pp; English.
                                                                                                                                                                                                                                                                      AAW85474 standard; Protein; 589 AA.
                                                                                                                                                                          1 EKAPAHLSLPDPQALKRDV 19
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970S-0863079,
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                                                                                                                                                                                                                                                                                                                                         (first entry)
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/note= "--
                                                                                                  Best Local Similarity 63.2
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                344..362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-045276/04.
                                                    179 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAV82824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
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23-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                         15-MAR-1999
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                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serrero G;
                                                                                                                                                                                                                                                                                                        AAW85474;
                                                                                    Query Match
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Mouse, granulin precursor, GP88; cytostatic; tumourigenicity; tamoxifen; antineoplastic; antioestrogen therapy; skin cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method for diagnosing tumourigenicity in a human. The method comprises obtaining a biological sample containing
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used as antigens to raise anti-GP88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-GP88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diagnosing tumorigenicity in a human, comprising obtaining a cell sample, detecting GP88 in the cells, and determining the number of positive cells in the sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used as antigens to raise
                                                                                                                                                                                                                                                                                                                                                             Mouse granulin/epithelin precursor (GP88) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACA.
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/note- "Encoded by ATG"
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/note= "Regions
antibodies"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Regions
antibodies"
                                                                                                                                                                                                            AAE20520 standard; Protein; 589
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                                                                     :| | | ||||| || |
344 KKVIAPLRLPDPQILKSD 361
                                          1 EKAPAHLSUPDPQALKRD 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            344..362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SERR/) SERRERO G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAD32849
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cells from the patient, detecting GP88 in the cells of the sample, and determining the number of GP88 positive cells in the sample, and determining the ratio of GP88 positive cells to the total number of cells in the sample. The invention also relates to a method for determining if a human patient is resistant to the antineoplastic effects of anticestrogen therapy. The method is useful for diagnosing tumourigenicity in a sample, such as blood, serum, plasma, urine, nipple aspirate, cerebrospinal fluid, liver, kidney, breast, bone, brain, lung, colon, or skin cancer. The method can be used to treat or prevent re-occurrence of cancer in a patient, by administering tamoxifen if the sample contains less than 10 % GP88, or less than 5 % GP88 positive cells. The present sequence is mouse granulin/epithelin precursor (GP88)
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                            Score 50; DB 23; Length 589;
Pred. No. 50;
L; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #28439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG28448 standard; Protein; 730 AA.
                                                                                                                                                                                                                                                                                                                                                                                                             1 EKAPAHLSLPDPQALKRD 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT;
                                                                                                                                                                                                                                                                                                            ch 51.0%;
1 Similarity 61.1%;
11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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N-PSDB; AAS92635.
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                                                                                                                                                                                                                                                                         589 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG28448;
                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                              Query Match
Best Local 9
                                                                                                                                                                                                                                       protein.
                                                                                                                                                                                                                                                                                                                                    Local
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disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and aliagnostic amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Whote: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                      DB 22; Length 730;
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Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; SEQ ID 14834; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashi K, Sa
A, Nagai K,
                                                                                                                                                                                                                                                                            43.8%; Pred. No. 89;
tive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human protein sequence SEQ ID NO:14834.
                                                                                                                                                                                                                                                          50.0%; Score 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB94335 standard; Protein; 324 AA.
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Sugiyama T, Wakamatsu
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637 EAPSYIAVPDPSVLKQ 652
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2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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Best Local Similarity 43.0-
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                                                                                                                                                                                                                         730 AA;
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L1 - JAN - 2000;
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09-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
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         the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length AAH13613 to AAH13612 represent human cDNA sequences; AAB92446 to AAH13632 represent buman anino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
 oligonucleotide comprises at least 15 nucleotides and the combination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang D;
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peripheral nervous system; neuropathy; central nervous system; CNS; Alzhehmer's; Parkinson's disease; Huntington's disease; harbenestitc; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
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Zhang J;
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                                                                                                                                                                                                                    22; Length 324;
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Yang Y,
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Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                                                                                                   Score 47; DB 2
Pred. No. 71;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                  AAM39674 standard; Protein; 828 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human polypeptide SEQ ID NO 2819.
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J, Wang Z, Wehrman T, X
QA, Zhou P, Goodrich R,
                                                                                                                                                                                                                                                                                              |: | | | | || || ERPPVHDQLQDPRLLKR 191
                                                                                                                                                                                                                                                                             1 EKAPAHLSLPDPQALKR 17
                                                                                                                                                                                                                   48.0%;
52.9%;
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2000US-0598042.
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                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                          of the present invention.
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                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                       324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
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09-JUL-2000;
19-JUL-2000;
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29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leukaemia.
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Wang J, V
Zhao QA,
                                                                                                                                                                                                                                                                                                          175
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The invention relates to human nucleic acids (AAI57798-AAI61369) and

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        immunosuppressant and cytostatic activity. The polymoclectides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the juvention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous alorables, peripheral nervous and placelised neuropathis and central nervous system disease, such as Alzheimer's, parkinson's disease, Huntington's disease, ampotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses inclide the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an Oilgo-dr primer and an oilgonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                   ;
polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                Length 828;
                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hikawa T, Hayashi K, Saito K, Y
Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; SEQ ID 11690; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                DB 22;
2e+02;
                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                  Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein sequence SEQ ID NO:11690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB92977 standard; Protein; 828 AA.
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Sugiyama T, Wakamatsı
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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52.9%;
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                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 52.97
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                                                                                                                                                                                                                                                                  828 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; primer;
                                                                                                                                                                                                                                 specification.
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09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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11-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB92977;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
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complementary strand of a polynucleotide which comprises a 5-end sequence and an oligonucleotide which comprises a 5-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 1'-end sequence complementary to a oligonucleotide comprises at 15 nucleotides and the complementary to a the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length conva. The primers are useful for synthesising polynucleotides, the full-length convas. The primers allow obtaining of the full-length convas. The primers allow obtaining of the full-length convas as ally without any specialised methods. AAR03166 to AAR13628 and AAR13639 represent human amino acid sequences; and AAR13629 to AAR13632 represent oligonucleotides, all of which are used in the exemplification of an oligonucleotide comprising a sequence complementary to the of the present invention.

828 AA; Sequence

0; Gaps Query Match

48.0%; Score 47; DB 22; Length 828;
Best Local Similarity 52.9%; Pred. No. 2e+02;
Matches 9; Conservative 2; Mismatches 6; Indels

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1 EKAPAHLSLPDPQALKR 17

|: | | | ||: ||| 679 ERPPVHDQLQDPRLLKR 695

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Search completed: July 8, 2003, 16:24:16 Job time: 48.5 secs

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US-07-668-648-4

| Sequence 4, Application US/07668648
| Sequence 4, Application US/07668648
| Patent No. 341619-1
| GENERAL INFORMATION:
| APPLICANT: Shoyab, Mohammed
| APPLICANT: Plowman, Gragory D. TITLE OF INVENTION: MODULATING PROTEINS |
| TITLE OF INVENTION: MODULATING PROTEINS |
| TITLE OF INVENTION: MODULATING PROTEINS |
| TITLE OF SEQUENCES: 12 |
| TORRESPONDENCE ADDRESS: |
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                                                                                                                                                                                                              July 8, 2003, 16:21:00; Search time 11.6923 Seconds (Without alignments) 47.812 Million cell updates/sec
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Sequence 4, 1
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Sequence 4
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -08-431-333-8
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-08-991-862-3
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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PCT-US91-02321-6 JS-08-807-342B-8

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Patent No. 5965723
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 98; DB 2; Length 593;
Best Local Similarity 100.0%; Pred. No. 4.9e-08;
Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                         Length 593;
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                                                                                          100.0%; Score 98; DB 2; 1
11larity 100.0%; Pred. No. 4.9e-08;
Conservative 0; Mismatchan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/668,648 FILING DATE: 13-WAR-1991 ATTORNEY/AGENT INFORMATION: NAME: Mistock, S. Leslie REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,333
FILING DATE: 27-APR-1995
FILING TARE: 27-APR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/08991862 Patent No. 6309826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 5
FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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    ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-429-998-4
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
amino acid
                                                                                                           Query Match
Best Local Similarity
Matches 19; Conserva
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Patent No. 5885961
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION:
TITLE OF INVENTION: MODULATING PROFEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 593;
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TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Penals & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PATENTINE PATENTINE
MEDIUM TYPE: PATENTINE
COMPUTER: PATENTINE
SOFTWARE: PATENTINE
SOFTWARE: PATENTINE
APPLICATION NUMBER: US/08/429, 998
FILING DATE: 13-ARR-1991
ATTONEY/AGENT INFORMATION:
REGISTRATION NUMBER: 18, 872
REFERENCE/COCKET NUMBER: 156-161-999
                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19910819
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.9e-08;
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Best Local Similarity 100.0%; Pred. No. 4.9e-08
Matches 19; Conservative 0; Mismatches 0
                                                                                                                                                                                                                    NAME: Misrock, S. Leslie
REGISTRATION NUBBER: 18,872
REFERENCE,/DOCKET NUBBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
PETERFONE: (212)790-0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         346 EKAPAHLSLPDPQALKRDV 364
                                                                                                                                                                                                                                                                                                                 TELEFAX: (212)790-9090
TELEFAX: (212) 869-9741
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: AMINO ACID
TOPOLOGY: line---
MOLECUIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EKAPAHLSLPDPQALKRDV 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein US-07-668-648-4
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-429-998-4

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Agent No. 3*10.2
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Showman, Gregory D.
APPLICANT: Plowman, Gregory D.
APP
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APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROFEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,648
FILING DATE: 19910819
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: 1155 Avenue of the Americas
New York
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1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :| | ||||||| || || || 344 KKVTASLSLPDPQILKNDV 362
                           Sequence 2, Application US/07668648 Patent No. 5416192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,877
REFERENCE/DOCKET NUMBER: 56
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212)790-9090
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 589 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.3%;
68.4%;
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MEDIUM TYPE: Floppy disk
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Best Local Similarity 68.47
Best Local 31 Conservative
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; MOLECULE TYPE: protein
US-07-668-648-2
                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1.
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
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New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
STREET: 11
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US-08-429-998-2
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TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS FILE REPERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/08/991,862
CURRENT FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/863,862
EARLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 17
LENGTH: 593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 593;
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AURLICATION NUMBER: PCT/US91/02321
FILING DATE: 19910403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: EPTTHELINS: NOVEL CYST
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company
STREET: 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 98; DE
Best Local Similarity 100.0%; Pred. No. 4.5
Matches 19; Conservative 0; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application PC/TUS9102321
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: POOT, BITAN N.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: 0N00'
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346 EKAPAHLSLPDPQALKRDV 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               346 EKAPAHLSLPDPQALKRDV 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EKAPAHLSLPDPQALKRDV 19
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Best Local Similarity 100.0%;
Matches 19; Conservative 0
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TELEFAX: (206)448-4775
INPORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Human GP88 CDNA
US-08-991-862-17
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PCT-US91-02321-4
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STATE: Washington
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Gaps

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US/08/429,998

APPLICATION NUMBER:

RESULT 7

Length 589;

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                                                                                                                                                                                                                                                                                 , Gregory D.

EPITHELINS: NOVEL CYSTEINE-RICH GROWTH MODULATING PROTEINS
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APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
    Length 589;
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                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02321
                                                                                                                                                                                                                                                                                                                                                                             E: Bristol-Myers Squibb Company 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                   Sequence 2, Application PC/TUS9102321 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 8, Application US/07668648
; Patent No. 5416192
                                                                                                      344 KKVTASLSLPDPQILKNDV 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 KKVTASLSLPDPQILKNDV 362
                                                                                  1 EKAPAHLSLPDPQALKRDV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: POOr, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PELECOMMUNICATION INFORMATION
    64.3%;
milarity 68.4%;
Conservative
                                                                                                                                                                                                                                                            APPLICANT: Shoyab, Mohammed APPLICANT: Plowman, Gregory TITLE OF INVENTION: EPITHEL TITLE OF INVENTION: MODULAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 589 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 68.4
Watches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein PCT-US91-02321-2
                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-M
                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Washington COUNTRY: USA
Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3005 F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98121
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Patent No. 5965723
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed APPLICANT: Showman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RILING DATE: "APPR-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNET/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
                                                                                                                                                                                                                                                                                                                                                                                                        Score 63;
                                                           APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTONNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERNICE/DOCKET NUMBER: 5624-161-99
TELEPHONE: (212)790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EKAPAHLSLPDPQALKRDV 19
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                                                                                                                                                                                                                                                                                                                                                                                                      64.3%;
68.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
      27-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 589 amino acids
amino acid
GY: linear
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INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 589 amino acids
                                                                                                                                                                                                                                                                                   : 589 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 64.3
Best Local Similarity 68.4
Matches 13; Conservative
  FILING DATE: 27-APR-1
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein US-08-429-998-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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: New York
RY: USA
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STATE:
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Gaps
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APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROFEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                          Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 179;
                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.25
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Pred. No. 0.25;
                                                                                                        Score 53; DB 2
Pred. No. 0.25;
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                                                                                                                                              3; Mismatches
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: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,333
FILING DATE: 27-APR-1995
CIASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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118 KKAPAHLSLLDLGAVEGDV 136
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Sequence 8, Application US/08431333
; Patent No. 5965723
                                                                                                                                                                                 1 EKAPAHLSLPDPQALKRDV 19
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.1%;
                                                                                                        Query Match 54.1%;
Best Local Similarity 63.2%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 869-9741 (NEORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 179 amino acids TYPE: amino acid
LENGTH: 179 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 63.29
Matches 12; Conservative
                                         MOLECULE TYPE: protein US-08-429-998-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-431-333-8
                    amino acid
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Y: USA
                                      linear
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                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                              RESULT 13
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Patent No. 5885961
APPLICANT: Shoyab, Mohammed APPLICANT: Shoyab, Mohammed APPLICANT: Plowman, Gregory D. TITLE OF INVENTION: PPITHELINS: NOVEL CYSTEINE-RICH GROWTH TITLE OF INVENTION: MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 179;
                                                                               SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 53; DB 1
Pred. No. 0.25;
3; Mismatches
                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 5624-161-999 FELECOMMUNICATION INFORMATION:
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STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/668,648 FILING DATE: 13-MAR-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/429,998 FILING DATE: 27-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 KKAPAHLSLLDLGAVEGDV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EKAPAHLSLPDPQALKRDV 19
                                  COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                         TELEPHONE: (212)790-9090
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ. ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 179 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 63.2
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-07-668-648-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                   FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                    10036
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     COUNTRY:
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Search completed: July 8, 2003, 16:30:20 Job time: 12.6923 secs
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TITLE OF INVENTION: 86 KDA TUDORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 20996, 488 APPO01-A
CURRENT APPLICATION NUMBER: US/08/991,862
CURRENT FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/863,862
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Gregory D. EPITHELINS: NOVEL CYSTEINE-RICH GROWTH MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 179;
                                                                                                                                                                                                                           COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02321
FILING DATE: 19910403
                                                                                                      E: Bristol-Myers Squibb Company 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; SEQ ID NO 2

: LENGTH: 589

: TYPE: PRT

: ORGANISM: Mouse epithelin/granulin

US-08-991-862-2
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Patent No. 6309826
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: POOL, Brian W.
REGISTRATION NUMBER: 32,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)728-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 54.1%;
Best Local Similarity 63.2%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 179 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein PCT-US91-02321-8
                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-M
                                                                                                                                               CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 1'SOFTWARE: PatentIn Ver.
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                     TILE OF INVENTION:
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US-08-991-862-2
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Gaps

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Indels

Mismatches

1 EKAPAHLSLPDPQALKRD 18

Query Match 51.0%; Best Local Similarity 61.1%; Matches 11; Conservative

Score 50; DB 4; Length 589; Pred. No. 3.1;

OM protein - protein search, using sw model

July 8, 2003, 16:24:26; Search time 18.5128 Seconds (without alignments) 119.483 Million cell updates/sec Run on:

US-09-824-647-6 98

Title: Perfect score:

1 EKAPAHLSLPDPQALKRDV 19 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters: 445758 seqs, 116419773 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/cgn2_6/ptodata/2/pubpaa/70s10_NEW_PUB.pep /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep Ptodata/2/pubpaa/US08_NEW_PUB.pep: Ptodata/2/pubpaa/US08_PUBCOMB.pep: ptodata/2/pubpaa/US09_NEW_PUB.pep: todata/2/pubpaa/US07_PUBCOMB.pep /ptodata/2/pubpaa/US09_PUBCOMB /cgn2_6/ptodata/2/pubpaa/US07_ Published_Applications_AA:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 6, Appli			Sequence 6, Appl1	Sequence 6, Appli	Sequence 17, Appl	Sequence 1416, Ap	Sequence 2, Appli	~	7	Sequence 2, Appli	Sequence 2, Appl1	Sequence 51, Appl	Sequence 4, Appli	Segmence 27. Appl				
										-										
	QI	US-09-824-647-6	US-10-218-509-6	US-10-281-160-6	US-09-813-156-6	US-09-824-807-6	US-09-824-647-17	US-10-218-509-17	US-10-281-160-17	US-09-813-156-17	US-09-824-807-17	US-09-925-301-1416	US-09-824-647-2	US-10-218-509-2	US-10-281-160-2	US-09-813-156-2	US-09-824-807-2	US-09-364-847-51	US-10-208-948-4	TS-10-208-948-27
	DB	6	6	6	2	10	6	6	6	2	10	2	σ,	σ	6	2	2	6	6	6
	Query Match Length DB	19	19	19	19	13	593	593	593	593	593	621	589	589	289	589	589	712	2115	2150
æ	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	51.0	51.0	51.0	51.0	51.0	49.0	46.9	46.9
	Score	86	86	98	86	86	86	86	86	86	96	96	20	20	20	20	20	48	46	. 46
	Result No.	-	7	e	4	S	9	7	œ	5	10	11	12	13	14	15	16	17	18	19

Sequence 34773, A Sequence 3, Appl1 Sequence 31, Appl1 Sequence 5211, Appl Sequence 62, Appl Sequence 62, Appl Sequence 62, Appl Sequence 62, Appl Sequence 64, Appl Sequence 1283, Ap Sequence 1283, Ap Sequence 1283, Ap Sequence 1283, Ap Sequence 64, Appl Sequence 1718, Ap Sequence 1718, Ap Sequence 1718, Ap Sequence 1718, Ap Sequence 64, Appl
10 US-09-864-761-34773 9 US-09-824-64-7 9 US-0-281-160-3 9 US-10-281-160-3 10 US-09-813-156-3 10 US-09-813-156-3 10 US-09-813-156-3 10 US-09-812-42-521 9 US-09-912-268-22 9 US-10-161-572-6-2 9 US-10-128-714-3343 9 US-10-128-714-3343 9 US-10-128-714-3343 9 US-10-128-714-3343 9 US-10-128-714-3343 9 US-10-128-714-3343 9 US-10-128-714-3343 9 US-10-156-761-1557 9 US-09-810-156-761-19516 9 US-09-810-156-761-19516 9 US-09-810-156-761-19516 9 US-09-810-156-761-19516 9 US-09-810-156-761-19516 9 US-09-810-156-761-19516 9 US-09-810-156-761-19516 9 US-09-810-156-761-19516 10 US-09-810-156-761-19516 10 US-09-810-195-761-19516 10 US-09-810-195-105-105-105-105-105-105-105-105-105-10
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4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
01122222222222222222222222222222222222

ALIGNMENTS

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Gaps
                                                                 APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996 488/P001-A
FILE REFERENT APPLICATION NUMBER: US/19/824,647
CURRENT FILING DATE: 2001-04-04
PRIOR PILING DATE: EARLIER PILING DATE: 1998-08-17
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17
PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23
NUMBER: OF SEQ ID NOS: 17
SOFTWARR: PATENTING DATE: PATENTING DATE: 1997-05-23
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1)..(19)
OTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 98; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.8e-09;
Matches 19; Conservative 0; Mismatches 0; Indels
Sequence 6, Application US/09824647 Publication No. US20020183270A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKAPAHLSLPDPQALKRDV 19
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Sequence 6, Application US/10218509; Publication No. US20030092661A1; GENERAL INFORMATION: APPLICANT: Serrero, Ginette

RESULT 2 US-10-218-509-6

Wed Jul

us-09-824-647-6.rapb

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FILE REFERENCE: Z9996.488/P001-A
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TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REPERENCE: 29996-488/P001-A
CURRENT APPLICATION NUMBER: US/10/281,160
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: US/08/991,862
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 08/863,862
PRIOR FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : LOCATION: (1)..(19); OTHER INFORMATION: Internal peptide of human GP88 used to develop; OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody. US-10-281-160-6
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TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS FILE REFERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/10/218,509
CURRENT FILING DATE: 2002-08-15
                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)...(19)
OTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
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illarity 100.0%; Pred. No. 7.8e-09;
Conservative 0; Mismatches 0;
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100.0%; Pred. No. 7.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                       PRIOR APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 08/863,862
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFFWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/10281160 Publication No. US20030108950A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EKAPAHLSLPDPQALKRDV 19
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SOFTWARE: PatentIn Ver. 2.0
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Matches 19; Conserv
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                                                                                                                                                                                                                                                                                                                   NAME/KEY: PEPTIDE
LOCATION: (1)..(19)
OCHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1)...(19)
OTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody.
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TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REPERENCE: 2996.488/P001-A
CURRENT APPLICATION NUMBER: U5/09/824,807
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR PLICATION NUMBER: 08/991,862
PRIOR PLICATION NUMBER: 08/863,862
PRIOR APPLICATION NUMBER: 08/863,862
PRIOR PLILING DATE: 1997-05-23
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TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
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100.0%; Pred. No. 7.8e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
CURRENT APPLICATION NUMBER: US/09/813,156
                    CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1997-12-16
PRIOR PELING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
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Publication No. US20020183270A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09824807 Patent No. US20020094966A1
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Best Local Similarity 100.0
Matches 19, Conservative
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Matches 19; Conservative
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ORGANISM: Human granulin
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US-09-824-647-17
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                                                                                                                                                                       SOFTWARE: Pat
SEQ ID NO 6
LENGTH: 19
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Gaps

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Length 593; Indels

Score 98; DB 9; Pred. No. 3.8e-07;

Mismatches

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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 19; Conservative 0
; ORGANISM: Human GP88 cDNA
US-10-281-160-17
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Bublication No. US20030092661A1

GENERAL INFORMATION:

APPLICANT SETENCY

ITILE OF INVENTION:

FILE REFERENCE: 29996.488/P001-A

CURRENT APPLICATION NUMBER: US/10/218,509

CURRENT PILING DATE: 1090-08-15

PRIOR APPLICATION NUMBER: 08/991,862

PRIOR PLICATION NUMBER: 08/991,862

PRIOR PLICATION NUMBER: 08/991,862

PRIOR FILING DATE: 1998-08-17

PRIOR FILING DATE: 1998-08-17

PRIOR FILING DATE: 1998-05-23

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PATENTIN VET. 2.0
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Publication No. US20030108950al
GENERAL INFORMATION:
APPLICAMT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REPRESENCE: 2996.488/P001-A
CURRENT APPLICATION NUMBER: US/10/281,160
CURRENT PILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: US/08/991,862
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-05-23
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                      CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 2001-04-04
PRIOR APPLICATION NUMBER: EARLIER PRE: 1998-08-17
PRIOR PELING DATE: EARLIER FILING DATE: 1998-08-17
PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 2.0
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Pred. No.
      CURRENT APPLICATION NUMBER: US/09/824,647
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Best Local Similarity 100.0%;
Matches 19; Conservative 0
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                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Human GP88 cDNA
US-09-824-647-17
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LENGTH: 593
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LENGTH: 593
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APPLICANT: Serriero, Ginette
TTILE NEFERENCE: 2996.488/P001-A
CURRENT APPLICATION NUMBER: US/99/824,807
CURRENT APPLICATION NUMBER: US/99/824,807
CURRENT FILING DATE: 1097-104-04
PRIOR FILING DATE: 1997-12-16
PRIOR FILING DATE: 1997-12-16
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                     APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 2996.488/P001-A
CURRENT APPLICATION NUMBER: 02/09/813,156
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1997-12-16
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Pred. No. 3.8e-07;
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Pred. No. 3.8e-07;
; Mismatches 0;
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Patent No. US20020094966A1
GENERAL INFORMATION:
                                                                                                                                              Sequence 17, Application US/09813156
Patent No. US20020061859A1
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 593
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Best Local Similarity 100.
Matches 19; Conservative
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LENGTH: 593
TYPE: PR
ORGANISM: Human GP88 CDNA
US-09-824-807-17
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Matches 19; Conservative
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US-09-813-156-17
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APPLICATION NUMBER: 08/991,862
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APPLICANT: SETTERO, GINETLE
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 299964 488/P001-A
CURRENT APPLICATION NUMBER: 02/99/824,647
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,862
PRIOR PILING DATE: EARLIER FILING DATE: 1999-08-17
PRIOR PLING DATE: EARLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VET. 2.0
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TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29966.488/PODID-A
CURRENT APPLICATION NUMBER: US/10/218,509
CURRENT FILING DATE: 2002-08-15
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                                                                                        GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR APPLICATION NUMBER: 60/124,270
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Pred. No. 4e-07;
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Pred. No.
                                                        Sequence 1416, Application US/09925301
Patent No. US20020052308A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Mouse epithelin/granulin
US-09-824-647-2
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Publication No. US20030092661Al.
GENERAL INFORMATION:
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Publication No. US20020183270A1
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100.0%;
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il Similarity 61.1%;
11; Conservative
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NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PatentIn Ver. 2.0
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Matches 19; Conservative
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Best Local Similarity
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                                   US-09-925-301-1416
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Gaps
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TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMER: US/10/281,160
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMER: US/08/991,862
PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 1997-05-23
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TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: Z9996.488/F001-A
CURRENT APPLICATION NUMBER: US/09/813,156
CURRENT FILING DATE: 2001-03-21
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Pred. No. 10;
1; Mismatches
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Pred. No.
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PRIOR FILING DATE: 1997-12-16
PRIOR FILING DATE: 1997-12-16
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 589
                                                                                                                                                                           ; TYPE: PRT ; ORGANISM: Mouse epithelin/granulin US-10-218-509-2 ;
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US-10-281-160-2
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Patent No. US20020061859A1
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PRIOR APPLICATION NUMBER: 08/99
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 08/86
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN Ver. 2.0
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ilarity 61.1%;
Conservative
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61.1%;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 589
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Best Local Similarity 61.1
Matches 11; Conservative
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Best Local Similarity
Matches 11; Conserv
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0; Gaps Query Match 51.0%; Score 50; DB 10; Length 589; Best Local Similarity 61.1%; Pred. No. 10; Matches 11; Conservative 1; Mismatches 6; Indels

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Search completed: July 8, 2003, 16:31:42 Job time: 19.5128 secs

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GenCore version 5.1.6
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- protein search, using sw model OM protein July 8, 2003, 16:19:45; Search time 19.2436 Seconds (without alignments) 94.918 Million cell updates/sec Run on:

Title: Perfect score:

US-09-824-647-6 98 1 EKAPAHLSLPDPQALKRDV 19 Sednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

•		Description	granulin precursor	epithelin/granulin	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote		hypothetical prote	ribonuclease PH (r	protein F12A21.5 [epithelin/granulin	phosphate acetyltr	hypothetical prote	septum site-determ	hypothetical prote	murein hydrolase [PRR2 alpha - human	bacteriophage N4 a	secretion protein	probable 2,3-dehyd	hypothetical prote	probable calcium c	hypothetical prote	cysteine synthase	beta-arrestin 2 -	early ElB 49K prot	hetical p		early transcriptio
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		G	СУНО	B38128	T50513	696595	576322	I50372	H72559	T22911	H90221	н96700	C38128	G75563 ⁻	F82984	AH2237	C98263	AG3021	153960	B49351	B83053	T46668	T20892	T18770	T00051	564303	A59279	ERADC2	G87414	C43497	142517
		DB	-	7	7	N	7	7	7	0	7	7	7	7	7	7	6	7	7	7	7	ņ	7	7	7	7	7	H	7	7	-
		Match Length DB	593	583	1857	2143	37.4	260	187	223	248	464	589	722	619	366	406	406	478	990	129	488	701	1148	1956	393	410	438	558	710	710
ф	Query	Match	100.0	64.3	6.94	46.9	45.9	45.4	44.9	44.9	44.9	44.9	44.9	44.9	44.4	43.9	43.9	43.9	43.9	43.9	42.9	42.9	42.9	42.9	42,9	41.8	41.8	41.8	41.8	41.8	41.8
		Score	96	63	46	46	45	44.5	44	44	44	44	44	44	43.5	43	43	43	43	43	42	42	42	42	42	41	41	41	41	41	41
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early transcriptio	A8L protein - vari	hypothetical prote	VETF, 82K subunit	probable transport	SEC15 protein - ye	plasmid replicatio	ribulbse bisphosph	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical 10.4	cardiotrophin-1 -	cardiotrophin-1 -	hypothetical prote	ONA-3-methyladenin	
H36848	E72164	T28549	T37394	G02500	S07838	T08312	C96695	S 66705	A97468	AD2686	B64982	I49153	JC4645	S69835	DGECMA	
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710	710	710	710	745	910	1128	2149	408	95	95	96	203	203	278	282	
41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.3	40.8	. 40.8	40.8	40.8	40.8	40.8	40.8	
. 41	41	41	41	41	41	41.	41	40.5	40	40	40	40	40	40	40	
30	3.2	32	33	34	35	36	37	38	39	0	41	42	43	44	5	

ALIGNMENTS

A; Reference number: A38128; MUID: 92317004; PMID: 1618805

A; Molecule type: mRNA A; Residues: 1-593 <PLO> Status: preliminary

A;Cross-references: GB:X62320; NID:931192; PIDN:CAA44196.1; PID:931193
R;Bhandari, V.; Palfree, R.G.E.; Bateman, A.
Proc. Natl. Acad. Sci. US.A. 89, 1715-1719, 1992
A;Title: Isolation and sequence of the granulin precursor cDNA from human bone mathematics and sequence of the granulin precursor cDNA from human bone mathematics. A;Reference number: A38118; MUID:92179253; PMID:1542665

A; Accession: A38118

A; Molecule type: mRNA A; Residues: 1-406, 'R', 408-433, 'G', 435-453, 'G', 455-459, 'O', 461-546, 'A', 548-566, 'R' A; Cross-references: GB:M75161; NID:g183612; PINN:AAA58617.1; PID:g183613 A; Note: this sequence has been revised in reference JC1284 A; Note: this sequence has been revised in reference C.; Solomon, S. Biochem: Blochem: Blochem: 173, 1161-1168, 1990 A; Title: Granulins, a novel class of peptide from leukocytes. A; Reference number: A36698; MUID:91097544; PMID:2268320

Molecule type: protein Residues: 281-336 <BAT> Note: this protein was purified and characterized as granulin Accession: B36698

Molecule type: protein Residues: 206-218, H', 220-233 <BA2> Note: this protein was purified and characterized as granulin Accession: C36698

A;Molecule type: protein A;Residues: 364-367, 'X',369-385,'H',387-396 <BA3> A;Note: this protein was purified and characterized as granulin C A;Accession: D36698

A;Molecule type: protein A;Residues: 442-446,'XDTSS',456-458,'DG' <BA4>

Gaps

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Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Al Chin, C.W.; Ching, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Al; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Ki C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitt, R.; Marz Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tal A;Attle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference onumber: A86141; MUID:21016719; PMID:11130712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, submitted to the Protein Sequence Database, May 2000
A;Reference number: 225102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GB:AE005173; NID:g10645420; PIDN:AAG21537.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F7A10.23 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein T27115_10 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Jul-2000.#sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
                                               A;Residues: 1-200,'S',203-388,'M',390-589 <RES>
A;Cross-references: GB:M97750; NID:g204223; PIDN:AAA16903.1; PID:g204224
C;Superfamily: granulin
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A;Experimental source: cultivar Columbia; BAC clone T27115
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97;
                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-200,'S',203-388,'M',390-589 <RES>
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Pred. No. 0.044;
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ed. No. 83;
Mismatches
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Pred. No.
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Pred. No.
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1336 EAPAHPAPPAPPLRRD 1352
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Local Similarity 68.4%;
les 13; Conservative
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ilarity 52.9%;
Conservative
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A;Introns: 295/1; 320/1;
A;Note: T27115_10
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
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A; Molecule type: DNA
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   A; Accession: I53272
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Matches
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 20-Aug-1999
C;Accession: B38128; A36199; B36199; B36698; I55272
R;Plowman, G.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Todaro, G.J.
A; Biol. Chem. 267, 13073-13078, 1992
A;Title: The epithelin precursor encodes two proteins with opposing activities on epithe
A;Reference number: A38128; MUID:92317004; PMID:1618805
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R;Shoyab, M.; McDonald, V.L.; Byles, C.; Todaro, G.J.; Plowman, G.D.
Proc. Natl. Acad. Sci. U.S.A. 87, 7912-7916, 1990
A;Title: Epithelins 1 and 2: Isolation and characterization of two cysteine-rich growth-A;Reference number: A36199; MUID:91045907; PMID:2236009
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A; Residues: 279-307, SB', 310-324, 'T', 326, 'X', 328, 'Q' <BAT>
A; Residues: 279-307, SB', 310-324, 'T', 326, 'X', 328, 'Q' <BAT>
R; Bhandari, V.; Giald, A.; Bateman, A.
Endocrinology 133, 2682-269, 1993
A; Title: The complementary deoxyribonucleic acid sequence, tissue distribution, and cell
A; Reference number: 153272; MUID:94062640; PMID:8243292
                                                                                                                                                                                                                                                                                                                                                                A;Map position: 17pter-17gter
A;Introns: 46/3; 88/3; 117/1; 154/3; 200/1; 236/3; 279/1; 311/3; 393/3; 471/3; 548/3
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                                  Br. J. Cancer 67, 686-692, 1993
A;Title: Characterisation of UGP and its relationship with beta-core fragment.
A;Reference number: A56873; MUID:93229246; PMID:8471426
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Bagshawe, K.D.; Coles, B.; Read, D.; Taylor, M.
7, 686-692, 1993
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A;Title: Granulins, a novel class of peptide from leukocytes.
A;Reference number: A36698; MUID:91097544; PMID:2268320
A;Accession: E36698
                                                                                                                                             A; Molecule type: protein
A; Residues: 281-283, 'X', 285-289, 'S', 291-295 <KAR>
A; Experimental source: urine
A; Note: sequence extracted from NCBI backbone (NCBIP:129524)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Keywords: glycoprotein; tandem repeat
F;1-17/Domain: signal sequence #status predicted <SIG>F;1-19/3/Product: granulin #status predicted <MAT>F;18-593/Product: progranulin #status predicted <PRO>F;18-594/Product: paragranulin #status experimental <PGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;123-179/Product: granulin F #status predicted <GRP>F;206-261/Product: granulin B #status experimental <GRB>F;281-316/Product: granulin A #status experimental <GRA>F;364-417/Product: granulin C #status experimental <GRA>F;442-496/Product: granulin D #status predicted <GRD>F;518-573/Product: granulin E #status predicted <GRB>
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Pred. No. 1.1e-07;
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A; Residues: 205-226 <SH2>
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Best Local Similarity
Matches 19; Conserv
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A; Residues: 1-589 <PLO>
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A.Gene: GDB:GRN
R;Kardana,
Br. J. Can
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Gaps

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A; Cross-references: DDBJ:AP000062; NID:g5105244; PIDN:BAA80765.1; PID:d1044551; f A; Experimental source: strain K1
A; Genetics:
A; Genetics: APE1762
C; Superfamily: Aeropyrum pernix hypothetical protein APE1762
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A;Experimental source: clone F58E10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F58E10.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 *sequence_revision 15-Oct-1999 *text_change 15-Oct-1999
C;Accession: T22911
R;McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ribonuclease PH (rph) (imported) - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
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                                                                                                                                                                                                                                  Score 44; DB 2; Length 187;
Pred. No. 13;
0; Mismatches 4; Indels
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A; Reference number: A99139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A: Status: preliminary; translated from GB/EMBL/DDBJ
A: Molecule type: DNA
A: Residues: 1-223 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, November 1996 A; Reference number: Z19637 A; Accession: T22911
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Pred. No. 18;
1; Mismatches
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C; Superfamily: tRNA nucleotidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||:| ||:| ||:| ||: ||: || 47 PAYLKLPNPEVAKQYV 62
                                                                                                                                                                                                                                  Best Local Similarity 71.4%;
Matches 10; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 PAHLSLPDPQALKRDV 19
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ilarity 56.2%;
Conservative
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90 HRSLPHPGALKRVV 103
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Matches 8; Conserve
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Best Local Similarity
Matches 9; Conserv
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A;Molecule type: DNA
A;Residues: 1-248 <KUR>
                                             A; Molecule type: DNA
A; Residues: 1-187 <KAW>
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A; Introns: 64/3; 166/1
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A;Gene: CESP:F58E10.6
                            A;Status: preliminary
A; Accession: H72559
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A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A; Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                        R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Sinmpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:D64000; GB:AB001339; NID:g1001484; PIDN:BAA10174.1; PID:g100154
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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R; Funahashi, J.; Sekido, R.; Murai, K.; Kamachi, Y.; Kondoh, H.
Development 119, 433-446, 1993
A; Title: Delta-crystallin enhancer binding protein delta EF1 is a zinc finger-homeodomai A; Reference number: I50222; MUID: 9411644; PMID: 7904558
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C:Accession: S76322
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C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 05-May-2000
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C;Accession: H72559
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C;Superfamily: CHD-1 protein; chromobox homology
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     Indels
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                                                                                                                                                                          C:Species: Synechocystis sp. (strain PCC 6803) Avariety: PCC 6803 C:Date: Aracety: PCC 6803 C:Date: Aracety: PCC 6803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: S74322; MUID:97061201; PMID:8905231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: 150372
A; Status: preliminary: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-560 <FUN>
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55.0%; Pred. No. 38;
tive 2; Mismatches
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  Mismatches
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ELAPLHKSIPSDPEERKRYV 487
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339 RPPVHLDLPDPSKM 352
                                                                                 372 HLSITDPSAARD 384
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Best Local Similarity 55.09
Matches 11; Conservative
                                                6 HLSLPDPQALKRD 18
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Best Local Similarity 50.0°
Matches 7; Conservative
8; Conservative
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A; Residues: 1-374 <KAN>
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A; Status: preliminary
Matches
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........ rurillcation of an autocrine growth factor homologous with mouse epithelin A;Reference number: A46705; MUID:93266526; PMID:8496151
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 18-19,'X',21-25,'X',27-29,'XX',32;'XXX',119-127;152-154,'DXK',158-161,'
C; Superfamily: granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: G75563
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A;Experimental source: strain Rl
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A;Residues: 1-619 <STO>
A;Cross-references: GB:AE004942; GB:AE004091; NID:99951607; PIDN:AAG08684.1; GSPDB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: G75563 (R) White, O.; Elsen, J.D.; Dodson, M.; Shen, M.; Venathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
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Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphate acetyltrdnsferase (EC 2.3.1.8) - Deinococcus radiodurans (strain R1)
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C;Date: 15-Sep-2000 *sequence_revision 15-Sep-2000 *text_change 31-Dec-2000
C;Accession: F82984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            c;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 *sequence_revision 03-Dec-1999 *text_change 09-Jun-2000
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60;
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48;
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Pred. No. 61;
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C.Keywords: acyltransferase; coenzyme A
                                                                                                                                                                                                                                                                                         Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EKAPAHLSLPDPQALKRD 18
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56.2%;
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RAVAHLTTPDPIPLTR 90
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Best Local Similarity 55.6%;
Matches 10; (Conservative
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Matches 9; Conservative
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H96700

protein F12A21.5 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: H96700
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, R.; ansen, N.F.; Hudbes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Lurcs, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A66141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
C138128
epithelin/granulin precursor - mouse
epithelin/granulin precursor - mouse
N.Alternate names: acrogranin; PC-cell-derived growth factor
C.Species: Mus musculus (house mouse)
N. Biol. Chem. C367, 13073-13078, 1993
A.Ribia: The epithelin precursor encodes two proteins with opposing activities on epithe
A.Reference number: A38128; MUD:92317004; PMID:1618805
A.Molecule type: mRNA
A.Residues: 1-589 < PLO>
A.Residues: 1-589 < PLO>
A.Residues: 1-589 < PLO>
A.Remoto, H.; Watenabe, K.; Aral, Y.; Gerton, G.L.
R.Baba, T.; Nemoto, H.; Watenabe, K.; Aral, Y.; Gerton, G.L.
FEBS Lett. 322, 89-94, 1993
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A;Recession: S32503
A;Accession: S32503
A;Residues: 18-349, 'L', 351-589 <BAB>
A;Residues: 18-349, 'L', 351-589 <BAB>
Molecule type: DNA
A;Residues: 18-349, 'L', 351-243, 1993
A;Title: Acrogranin, an acrosomal cysteine-rich glycoprotein, is the precusor of the grd
A;Reference number: 148141; MUID:93228994; PMID:8471244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: mRNA
A;Nolecule type: mRNA
A;Residues: 1-250,'L','252-253,'V','255-349,'L','351-401,'SA',404-589 <RES>
A;Cross-references: GB:M86736; NID:g191766; PIDN:AAA37191.1; PID:g191767
R;Zhou, J.; Gao, G.; Crabb, J.W.; Serrero, G.
J. Biol. Chem. 268, 10863-10869, 1993
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Pred. No. 37;
2; Mismatches
                                                 EKAPAHLSLPDPQALK 16
                                                                             FMHPRHLSLPDRAVLR 78
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Conservative
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81 KRPAHLNIPDLNPQ 94
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Best Local Similarity
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M W.

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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki; N.; Shimpo, S.; Suglmoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2010
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein AGR_L_2112 [imported] - Agrobacterium tumefaciens (strain C58, Cere C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C; Accession: C98263
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                  A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
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A;Experimental source: strain PCC 7120
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Gaps
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Pred. No. 46;
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2; Mismatches
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Mismatches
3; Mismatches
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Pred. No.
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Job time.: 21.2436 secs
                                                                                                581 EAYPAHLRRMDLDDPQGLREEL 602
                                                1 EKAPAHL---SLPDPQALKRDV 19
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Best Local Similarity 52.9%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: AGR_L_2112
A;Map position: linear chromosome
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Best Local Similarity 77.8%;
Matches 7; Conservative
Conservative
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78 APAHINLPD 86
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A; Molecule type: DNA
A; Residues: 1-406 <KUR>
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A; Residues: 1-366 <KUR>
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Matches
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 8, 2003, 16:16:30; Search time 9.25641 Seconds (without alignments) 85.136 Million cell updates/sec Run on:

US-09-824-647-6 98 1 EKAPAHLSLPDPQALKRDV 19 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P28799 h granulins	P23785 r granulins	=	P31600 escherichia	Q9hv52 pseudomonas	035214 mus musculu	Q9jm98 mus musculu	P53206 saccharomyc	Q08339 erythrocebu		P14266 canine aden	015213 homo sapten		P20635 vaccinia vi	Q9jf93 vaccinia vi	P20636 vaccinia vi	P33806 variola vir	P33897 homo sapien	P22224 saccharomyc	P25040 saccharomyc	Q60753 mus musculu	Q63086 rattus norv	P04395 escherichia	_	P96115 treponema p	Q9ubr1 homo sapien	Q10609 mycobacteri	P12894 mouse intra	:014511 homo sapien	_	095613 homo sapten		P47930 mus musculu
		! !																			•			-							•	•		
	. aı	GRN_HUMAN	GRN_RAT	GRN_MOUSE	NFRA_ECOLI	SECG_PSEAE	OPSX_MOUSE	WDR8_MOUSE	CYSK_YEAST	CD4_ERYPA	ARR2_RAT	E1BL_ADECT	BIN4_HUMAN	ETF2_VACCA	ETF2_VACCC	ETF2_VACCT	ETF2_VACCV	ETF2_VARV	ALD_HUMAN	SC15_YEAST	YOC2_YEAST	CTF1_MOUSE	CTF1_RAT	3MG2_ECOLI	CG96_HUMAN	RUVB_TREPA	BUP1_HUMAN	SYR_MYCTU	POL_IPMAI	NRG2_HUMAN	NRG2_RAT	PCN2_HUMAN	FRA2_HUMAN	FRA2_MOUSE
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æ	Query Match	100.0	64.3	51.0	43.9	42.9	42.9	42.9	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.3	40.8	40.8	40.8	40.8	40.8	40.8	40.8	40.8	40.8	40.8	40.8	39.8	39.8
	Score		63	20	43	42	42	42	41	41	41	41	41	41	41	41	41	41	41	41	40.5	40	40	40	40	0.4	40	40	40	40	40	40	39	39
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			084713 chlamydia t									P35884 thiobacillu	
	FKAZ_KAI	GLXD_RHIME	TIG_CHLTR	ETF2_MYXVL	ARG2_YEAST	NID2_MOUSE	POLR_ELV	NOT1_YEAST	FA8_PIG	AMBP_PLEPL	ES1_HUMAN	TRA2_THIFE	
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6	37.8	39.8	39.8	39.8	39.8	39.8	39.8	39.8	39.8	39.3	38.8	38.8	
ć	3,5	39	39	39	. 39	39	36.	.39	39	38.5	38	38	•
;	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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RESULT 1

36	אניטרון ד אניטרון ד
QI QI	GRN HOMAN STANDARD: PRT: 593 AA.
AC	P28799; P23781; P23782; P23783; P23784; Q9BWE7;
5	01-NOV-1991 (Rel. 20, Created)
TO	01-DEC-1992 (Rel. 24, Last sequence update)
ξ	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Granulins precursor (Acrogranin) [Contains: Paragranulin; Granulin 1
DE	ᆸ,
DE	Granulin 4 (Granulin A); Granulin 5 (Granulin C); Granulin 6 (Granulin
DE	D); Granulin 7 (Granulin E)].
N S	GRN
SO	
8	<pre>Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostoml;</pre>
8	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
XO.	NCBI_TaxID-9606;
RN	(1)
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
2	TISSUE-Bone marrow;
RX	MEDLINE=92179253; PubMed=1542665;
RA RA	.E., Bateman A.;
RT	
RT	bone marrow reveals tandem cysteine-rich granulin domáins.";
RL	Proc. Natl. Acad. Sci. U.S.A. 89:1715-1719(1992).
RN	[2]
RP	REVISIONS; SEQUENCE FROM N.A.
XX	MEDLINE=93038704; PubMed=1417868;
Z.	Bhandari V., Bateman A.;
T.C	"Structure and chromosomal location of the human granulin gene.":
10	
2 8	for the property of the proper
Z ([3]
A 6	SEQUENCE FROM N.A.
2	TISSUE-KIQUEY
RX	MEDLINE-92317004; PubMed-1618805;
RA	Plowman G.D., Green I.M., Neubauer M.G., Buckley S.D., McDonald V.L.,
æ	Todaro G.J., Shoyab M.;
RT	"The epithelin precursor encodes two proteins with opposing activities
RT	on epithelial cell growth.";
R	J. Biol. Chem. 267:13073-13078(1992).
RN	[4]
RP	SEQUENCE FROM N.A.
RC RC	TISSUE-Brain;
RA	Yu W., Gibbs R.A.;
Z.	Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
RN	(5)
RP	
2	
æ	
RL	Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN	. [9]
RP	SEQUENCE OF 206-233; 281-336; 364-396 AND 442-447.
S i	TISSUE-Leukocyte;
ž	
£ :	
1 1	Granuins, a novel class of peptide from leukorytes;
<u>.</u>	BIOCHEM: BIOPNYS: Res. Commun. 1/3:1101-1100(1990).

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122
204
278
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                                                                                                                      TISSUE-Kidne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
FUNCTION: GRANULINS HAVE POSSIBLE CYTOKINE-LIKE ACTIVITY. THEY MAY PLAY A ROLE IN INFLAMMATION, WOUND REPAIR, AND TISSIE REMODELING. FUNCTION: GRANULIN A PROMOTES PROLIFERATION OF THE EPITHELIAL CELL. LINE A431 IN CUTFORE WHILE GRANULIN B ACTS AS AN ANTAGONIST OF GRANULIN B, INHIBITING THE GROWTH.

ALTERNATIVE PRODUCTS: 2 150forms; 1 (shown here) and 2; may be produced by alternative splicing.

TISSUE SPECIFICITY: IN MYELOGENOUS LEUKENIC CELL LINES OF PROMONOCYTIC, PRONYELCCYTIC, AND PRORYTHELIAL CELL LINES. PRESENT IN INFLAMMATORY CELLS AND BONE MARROW. HIGHEST LEVELS IN KIDNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL). (POTENTIAL). (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                    PROSITE; PS00799; GRANULINS; 7.
Cytokine; Repeat; Glycoprotein; Signal; Alternative splicing;
Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 593;
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W -> H (IN REF. 6).
4E402BDB16DE2819 CRC64;
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N-LINKED (GLCNAC...) (
N-LINKED (GLCNAC...)
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Pred. No. 5.9e-08;
; Mismatches 0;
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/FTIG=VAR_003445.
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GRANULIN 5.
GRANULIN 5.
GRANULIN 6.
GRANULIN 7.
                                                                                                                                                                                                                                                                                                                                                                              GRANULIN 1.
                                                                                                       PTM: GRANULINS ARE DISULFIDE BRIDGED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (N-LINKED (
                                                                                                                                                                                                                                                                                                                                                                                        GRANULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                              EMBL; M75161; AAA58617.1; ALT_SEQ.
EMBL; X62320; CAA44196.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKAPAHLSLPDPQALKRDV 364
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                                                                                                                                                                                                                                                                                             InterPro; IPR000118; Granulin.
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SMART; SM00277; GRAN; 7.
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Best Local Similarity 100...
The 19; Conservative
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386
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MIM; 138945; -.
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PIR; D36698; D36698.
PIR; JC1284; JC1284.
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593 AA;
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P23785;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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-!- FUNCTION: GRANULINS HAVE POSSIBLE CYTOKINE-LIKE ACTIVITY. THEY MAY PLAY A ROLE IN INFLAMMATION, WOUND REPAIR, AND TISSUE REMODELING.
-!- TISSUE SPECIFICITY: UBIQUITOUS; MOST ABUNDANT IN THE SPLEEN AND SEVERAL TISSUES OF ENDOCKINE SIGNIFICANCE.
-!- PTM: GRANULINS ARE DISULFIDE BRIDGED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plowman G.D., Green J.M., Neubauer M.G., Buckley S.D., McDonald V.L., Todaro G.J., Shoyab M.;
"The epithelin precursor encodes two proteins with opposing activities on epithelial growth.";
J. Biol. Chem. 267:13073-13078(1992).
                                                                                                                                                                                                                                                                                                 Eukaryota; "Metazoa; Chordata; Craniata; Vertebrata; Euteleoŝtomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID-10116;
                                                                                  (Granulin G);
01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Granulins precursor (Acrogrania) [Contains: Granulin 1 (Granulin 2 (Granulin P); Granulin 3 (Granulin B) (Epithelin 2);
Granulin 4 (Granulin A) (Epithelin 1); Granulin 5 (Granulin C);
Granulin 6 (Granulin D); Granulin 7 (Granulin E)].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE-91045907; PubMed-2236009; Shoyab M., McDonald V.L., Byles C., Todaro G.J., Plowman G.D.; Shoyab M., McDonald V.L., Byles C., Todaro G.J., Plowman G.D.; Epithellins 1 and 2: isolation and characterization of two cysteine-rich growth-modulating proteins."; Proc. Natl. Acad. Sci. U.S.A. 87:7912-7916(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94062640; PubMed-8243292;
Bhandari V., Giaid A., Bateman A.;
The complementary deoxyribonucleic acid sequence, tissue
distribution, and cellular localization of the rat granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 204-259 AND 278-334
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ACROGRANIN.
GRANDLIN 1.
GRANDLIN 2.
GRANDLIN 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92317004; PubMed=1618805;
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MEDLINE-91097544; PubMed-2268320;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 204-225 AND 279-299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000118; Granulin. Pfam; PF00396; granulin; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M97750; AAA16903.1; -. EMBL; X62322; CAA44198.1; -.
                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
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PIR; B36199; B36199.
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for commercial
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MEDLINE-92317004; PubMed-1618805;
MEDLINE-92317004; PubMed-1618805;
MEDLINE-92317004; PubMed-1618805;
MEDLINE-92317004; Medium of the structure 
                                                                                                                                                                                                                                                                                                                                                    Gaps
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Granulins precursor (Acrogranin) [Contains: Granulin 1; Granulin 5; Granulin 5; Granulin 7].
                                                                                                     (POTENTIAL).
                                                                              (POTENTIAL)
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                                                                                                                                                                                                                                                                                            Score 63; DB 1; Length 588;
Pred. No. 0.021;
1; Mismatches 5; Indels
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"Exon'Intron organization of the gene encoding the mouse
epithelin/granulin precursor (acrogranin).";
FEBS Lett. 322:89-94(1993).
GRANULIN 5.
GRANULIN 6.
GRANULIN 6.
GRANULIN 6.
GRANULIN 7.
N-LINKED (GLCNAC. . .) (POTI)
N-LINKED (GLCNAC. . .) (POTI)
S -> FP (IN REF. 2).
TK -> SB (IN REF. 4).
O -> T (IN REF. 4).
M -> I (IN REF. 2).
H -> I (IN REF. 2).
W, 113D434F7E099831 CRC64;
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Cytokine; Repeat; Glycoprotein; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                        343 KKVTASLSLPDPQILKNDV 361
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SMART; SM00277; GRAN; 7.
PROSITE; PS00799; GRANULINS:
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EMBL; X62321; CAA44197.1;
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588 AA;
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P28798;
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Ikemoto K., Inada T., Itoh T., Rajihara M., Ranai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=KIZ - MG165;
STRAIN=KIZ - MG165;
STRAIN=KIZ - MG165;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Riley M., Collado-Vides J., Glasner H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
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Ching E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin
Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                               (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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Escherichia.
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"Two overlapping genes encoding membrane proteins required for bacteriophage N4 adsorption.";
J. Bacteriol. 175:7081-7085(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fano M., Horiuchi T.;
A 718-kb DNA sequence of the Escherichia coli K-12 genome
                                                                                                                                                                                                  Score 50; OB 1; Length 589;
Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                 6; Indels
                                                                                                                                                                  -> R (IN REF. 2).
1DE8229C413CB787 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Bacterlophage N4 adsorption protein A precursor
NFRA OR B0568.
                                                                                                               N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                        (GLCNAC.
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                                                                                                                                                                               MW.
                                                                                                                                                                                                       51.0%;
61.1%;
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Atches 11; Conservative
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589. AA;
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                                                                                                                                                                                                         Query Match
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              CHAIN
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
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                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
-1- FUNCTION: REQUIRED FOR BACTERIOPHAGE N4 ADSORPTION. SERVES AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-ATCC 15692 / PRO1;
MEDLINE-20437337; PubMed=10984043;
MEDLINE-20437337; PubMed=10984043;
Stover C.R., Pham X. Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.
Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Polger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- FUNCTION: INVOLVED IN PROTEIN EXPORT. PARTICIPATES IN A EARLY EVENT OF PROTEIN TRANSLOCATION (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACTERIOPHAGE N4 ADSORPTION PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phage recognition; Outer membrane; Signal; Complete proteome. SIGNAL 1 27 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.9%; Score 43; DB 1; Length 990; 56.2%; Pred. No. 54; tive 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     990 AA; 111307 MW; AAA616665D1C2E72 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-0cT-2001 (Rel. 40, Created)
16-0cT-2001 (Rel. 40, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
Protein-export membrane protein secG.
SECG OR PA4747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (By similarity).
--- SIMILARITY: BELONGS TO THE SECG FAMILY.
                                                                                                                                                  SUBCELLULAR LOCATION: Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AE000161; AAC73669'1; -. U82598; AAB40766.1; -. D90699; BAA35202.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||| ||| || || 671 PAHKGLPDDPALIRQL 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; 116945; AAC36849.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 PAHLSLPDPQALKRDV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001440; TPR. Pfam; PF00515; TPR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 56,2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; B49351; B49351.
EcoGene; EG11740; nfrA.
                                                                                                                    PHAGE RECEPTOR. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECG_PSEAE
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SECG_PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID-10090;
                                                                              Tickrams; iloruvolu, secc, 4.
Protein transport; Translocation; Transmembrane; Inner membrane;
                                                                                                                                                                        Score 42; DB 1; Length 129; Pred. No. 8.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN 1 26 EXTRACELLULAR.
TRANSMEM 27 49 1 (POTENTIAL).
                                                                                                                , 5 25 POTENTIAL.
56 76 POTENTIAL.
129 AA; 13207 MW; CIEFBBB2A3D52634 CRC64;
                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Visual pigment-like receptor peropsin.
                                                                                                                                                                                                                                                                                                                                    337 AA
                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00001; 7tm_1; 1.

PROSITE; PS00231; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50052; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS00238; OPSIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:1097709; Rrh.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR001760; Opsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Retina;
MEDLINE-97420780; PubMed-927522;
                                                                                                                                                                                                                                                            77 EKSDALQHIGLPDPAVLEQ 95
                                                                                                                                                                                                                               1 EKAPA--HLSLPDPQALKR 17
                                             EMBL; AE004888; AAG08133.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF012271; AAC53344.1; -.
                                                                                                                                                                         42.98;
                                                                                                                                                                                        47.48;
                                                         InterPro; IPR004692; SecG.
TIGREAMS; TIGR00810; SecG;
                                                                                                                                                          Query Match (arity 4/.... Best Local Similarity 4/.... 9; Conservative
                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPSIN SUBFAMILY.
                                                                                                 Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    OPSX_MOUSE
035214;
                                                                                                                TRANSMEM
TRANSMEM
SEQUENCE
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393 AA; 42801 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.8%;
                                                                                        Similarity 47.4%;
9; Conservative
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|34 AHISLPDDTSLEK 146
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Best Local Similarity 53.0.
The Transfer Conservative
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                                                                                                                                                                                                                                                                                    STANDARD;
                                     462 AA;
                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                CYSK_YEAST
P53206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                     SEQUENCE
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REPEAT
                   REPEAT
                                                                                                                                                                                                                                                                CYSK_YEAST
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CD4_ERYPA
                                                                                                                Matches
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"Isolation, characterization, and mapping of the mouse and human WDR8 genes, members of a novel WD-repeat gene family.";
Genomics 72:252-259(2001).
-!- SUGCELICHIAR LOCATION: Cytoplasmic (Potential).
-!- TISSUE SPECIFICITY: Ubiquitous.
-!- TISSUE SPECIFICITY: Obiquitous.
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 1; Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                    7; Indels
                                                                                                                                                                                                                                                                                                                         353E4E2278EDBFA6 CRC64;
                                                                                                                                                                                                                                                                                        POTENTIAL.
RETINAL CHROMOPHORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro: IPR001680; WD40.
Pfam; PF00400; WD40; 3.
SMARY; SM00320; WD40; 2.
PROSITE; PS00678; WD_REPEATS_1; FALSE_NEG.
PROSITE; PS50082; WD_REPEATS_2; FALSE_NEG.
PROSITE; PS50082; WD_REPEATS_REGION; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2002 (Rel. 41, Last annotation update)
WD-repeat protein 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            462 AA.
                                                                                            4 (POTENTIAL).
EXTRACELLULAR.
5 (POTENTIAL).
                                                       3 (POTENTIAL).
CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 24; ; Mismatches
                   2 (POTENTIAL)
EXTRACELLULAR
                                                                                                                                                     CYTOPLASMIC.
6 (POTENTIAL)
                                                                                                                                                                                           EXTRACELLULAR
                                                                                                                                                                                                               7 (POTENTIAL)
                                                                                                                                                                                                                                CYTOPLASMIC
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1.28.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 KAPAHLSLPDPQALKRDV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB034911; BAA92311.1; -.
                                                                                                                                                                                                                                                                                                                           37208 MW;
                                                                                                                                                                                                                                                                                                                                                               42.98;
                                                                                                                                                                                                                                                                                                                                                                                ilarity 38.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
Les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                         337 AA;
                                                                                                                                                                                                                                                                  182
98
284
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                                                                                                                                                                                                                              DOMAIN
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                    DISULPID
BINDING
SEQUENCE
DOMAIN
                                       DOMAIN
TRANSMEM
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TRANSMEM
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TRANSMEM
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REPEAT
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                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
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                                                                                                                                                                           Gaps
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-i- PATHWAY: Cysteine biosynthesis.
-i- SIMILARITY: BELONGS TO THE CYSTEINE SYNTHASE/CYSTATHIONINE BETA-
SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-S288C;
MEDLINE-97435481; PubMed-9290212;
Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.;
Riegerence analysis of 203 kilobases from Saccharomyces cerevislae chromosome VII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYRIDOXAL PHOSPHATE (BY SIMILARITY). 76C73396D77B69AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       reast 13:1077-1090(1997).
-!- CATALYTIC ACTIVITY: 03-acety1-L-serine + H(2)S = L-cysteine
                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                               Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative cysteine synthase (EC 4.2.99.8) (O-acetylserine sulfhydrylase) (C-acetylserine (Thiol)-lyase) (CSASE).
369 WD 5.
410 WD 6.
52026 MW; 0142524BB1801D51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00901; CYS_SYNTHASE; 1.
Hypothetical protein; Lyase; Cysteine biosynthesis;
Pyridoxal phosphate.
                                                                                                                  42.9%; Score 42; DB 1; 47.4%; Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                       393 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred, No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGD; SO003244; YGR012W.
InterPro: IPR001926; B6_enzyme_beta.
InterPro: IPR001216; Cys_synthase.
Pfam; PF00291; PALP: 1
                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                     1 EKAP----AHLSLPDPQAL 15
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Wed Jul

397 AA

PRT;

STANDARD;

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family.
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                                                                 P29067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (BY SIMILARITY).
                                                                                                                                                                                                                             Fonsgaard A., Hirsch V.M., Johnson P.R.; "Cloning and sequences of primate CD4 molecules: diversity of the cellular receptor for simian immunodeficiency virus/human
                         01-FEB-1995 (Rel. 31, Created)
1-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
T-cell surface glycoprotein CD4 (T-cell surface antigen T4/Leu-3)
                                                                                                       Erythrocebus patas (Red guenon) (Hussar).
Busdrycher; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Erythrocebus.
                                                                                                                                                                                                                                                                   Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;
Immune response; Repeat; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 1; Length 397;
Pred. No. 41;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PALMITATE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44081 MW; 67887397A6B7EA4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY
                                                                                                                                                                                                                 MEDLINE-93049640; PubMed-1425921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003006; Ig_MHC.
InterPro; IPR003600; Ig_like.
InterPro; IPR003596; Ig_v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X73324; CAA51750.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00410; IG_like; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           395
397
397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 Similarity
10; Consery
                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                             NCBI_TaxID=9538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047
                                                                              (Fragment).
CD4_ERYPA
008339:
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DOMAIN
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SEQUENCE
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Best Local
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DOMAIN
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                                                                                                                           Rattus norvėgicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eitheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUT. J. Neurosci. 10:2607-2616(1998).
-I- FUNCTION: REGULATES BETA-ADRENERGIC RECEPTOR FUNCTION. BETA-ADRENERGIC RECEPTORS, ARRESTINS SEEM TO BIND PHOSPHORYLATED BETA-ADRENERGIC RECEPTORS, THEREBY CAUGING A SIGNIFICANT IMPAIRMENT OF THEIR CAPACITY TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIVATE G(S) PROTEINS.
TISSUE SPECIFICITY: PREDOMINANTLY LOCALIZED IN NEURONAL TISSUES
AND IN THE SPLEEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 beta-arrestin-1 and -2 in rat central nervous system and peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                            Craft C.M., Whitmore D.H., Wiechmann A.F.; "Cone arrestin identified by targeting expression of a functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                  STRAIN-Sprague-Dawley; TISSUE-Brain; MEDLINE-92388146; PubMed=1517224; Attramadal H., Arriza J.L., Rokl C., Dawson T.M., Codina J., Kwatra M.M., Shyder S.H., Caron M.G., Lefkowitz R.J.; Beta-arrestin2; a novel member of the arrestin/beta-arrestin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Sprague-Dawley; TISSUE-Retina;
MEDINE-99145674; PubMed-996731;
Komori N., Cain S.D., Roch J.-M., Miller K.E., Matsumoto H.;
"Differential expression of alternative splice variants of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46340 MW; ODFA6A897C2B86BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE ARRESTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB 1;
Pred. No. 42;
5; Mismatches
                              01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-GRA-arrestin 2 (Arrestin, beta 2).
410 AA.
                                                                                                                                                                                                               <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.8%; Score 41; 42.9%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                        nily.";
Biol. Chem. 267:17882-17890(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 269:4613-4619(1994).
                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Pineal gland;
MEDLINE-94140898; PubMed-8308033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD002099; Arrestin; 1. PROSITE; PS00295; ARRESTINS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000698; Arrestin.
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 295-410 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 305-386 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00339; arrestin; 1.
Pfam; PF02752; arrestin_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M91590; AAA74460.1; -. EMBL; U03627; AAA17551.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF051457; AAC28617.1;
HSSP; P08168; 1CF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00309; ARRESTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sensory transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               410 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissues.
                                                                                                                                                                                                                       SEQUENCE
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Gaps

5

11 | ||:| |||| 249 EKLPLHLTL--PQAL 261

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1 EKAPAHLSLPDPQAL 15 Conservative

Matches

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Pfam; PF00400; WD40; 1.
                                                                                                                                                               SMART; SM00320; WD40;
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
'-hes 9; Conserve
                                                                                                                                                                                                                                                                                      610 AA;
                                                                                                                                                                                                           Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=126794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          late genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ETF2_VACCA
                                                                                                                                                                                                                                                                                                                                                                             507
                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                               REPEAT
REPEAT
                                                                                                                                                                                                                                                        REPEAT
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ETF2_VACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herberg J.A., Beck S., Trowsdale J.;
"TAPASIN, DAXX, RGL2, HKE2 and four new genes (BING 1, 3 to 5) form
dense cluster at the centraric end of the MHC.";
J. Mol. Biol. 277:839-857(1998).
                                                                                              01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ElB protein, large T-antigen (Early ElB 49 kDa protein).
Canhe adenovirus type 2 (strain Toronto A 26-61).
NTRUSES; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxID=9606;
                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-90021176; PubMed-2800332;
Shibata R., Shinagawa M., Ilda Y., Tsukiyama T.;
"Nucleotide sequence of El region of canine adenovirus type 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ÷.
                                                                                                                                                                                                                                                                                                                                                                                                                                  41.8%; Score 41; DB 1; Length 438; 62.5%; Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                             438 AA; 48865 MW; 4A7B9ABA4548421B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
M5-Tepeat protein BING4.
CGORFI1 OR BING4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        610 AA.
                                                                                     438 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002612; AdenoE1B_55kDa.
Pfam; PF01696; Adeno_E1B_55K; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-98213668; PubMed-9545376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 LSLPDP----QALKRD 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         353 HITLPRPOSAPREI 366
          HLSLPDPQALKRDV 19
                                                                                                                                                                                                                                           Virology 172:460-467(1989)
                                                                                                                                                                                                                                                                                                                                                      EMBL; J04368; AAA42472.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                   PIR; C34165; ERADC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                    Early protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIN4_HUMAN
015213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rISSUE-Lund;
                                                                                     E1BL_ADECT
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
                                                                RESULT 11
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                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
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Antoine G., Scheiflinger F., Dorner F., Falkner F.G.;
"The complete genomic sequence of the modified vaccinia Ankara strain:
comparison with other orthopoxviruses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 87:4401-4405(1990).
-!- FUNCTION: ACTS WITH RNA POLYMERASE TO INTITATE TRANSCRIPTION FROM
EARLY GENE PROMOTERS. A DNA-DEPENDENT ATPASE ACTIVITY IS
ASSOCIATED WITH VETF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gershon P.D., Moss B.;
"Early transcription factor subunits are encoded by vaccinia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Early transcription factor 82 kDa subunit (VETF large subunit).
MVA1181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: HETERODIMER OF A 70 kDa AND A 82 kDa SUBUNIT.
-1- SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OC11DA8EDCBA3DEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           710 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00678; WD_REPEATS_1; FALSE_NEG.
PROSITE; PS50082; WD_REPEATS_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.8%; Score 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS50294; WD_REPEATS_REGION; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION.
MEDLINE-90272720; Pubmed-2190222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last seq
16-0CT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccinia virus (strain Ankara)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68041 MW;
                                                                                                                                                                                                                                                                                                         EMBL; 297184; CAB09994.1; -. EMBL; BC000388; AAH00388.1; Genew; HGNC:13923; CGorf11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             || || || | || || || || || || || EKVPAELICLDPRAL 521
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                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Appendix to 'The complete DNA sequence of vaccinia virus'.";
Virology 179:517-563(1990).
-!- FUNCTION: ACTS WITH RNA POLYMERASE TO INITIATE TRANSCRIPTION FROM
EARLY GENE PROMOTERS. A DNA-DEPENDENT ATPASE ACTIVITY IS
ASSOCIATED WITH VETF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                    Vaccinia virus (strain Copenhagen).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
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  and for
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9
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                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Last annotation update)
Early transcription factor 82 kDa subunit (VETF large subunit).
                                                                                                       SUBUNIT: HETERODIMER OF A 70 kDa AND A 82 kDa SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 1; Length 710;
Pred. No. 77;
7; Mismatches 4; Indels
 .Usage by
                                                   EMBL; U94848; AAB96460.1; -.
Transcription regulation; Activator; Late protein.
SEQUENCE 710 AA; 82330 MW; E3DCF437C4C66AFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcription regulation; Activator; Late protein.
SEQUENCE 710 AA; 82329 MW; F9683BC45B3F0C67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete DNA sequence of vaccinia virus.";
Virology 179:247-266(1990).
                                                                                                                                                                                                                                                           710 AA.
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modified and this statement is not removed. entities requires a license agreement (See Por send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                (Rel. 17, Last sequence update) (Rel. 40, Last annotation update
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                                                                                                                                                                               ||:| :| :||: || EKSPIYFLRSHLNIQQPEIVKRH1 57
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-91021027; Pubmed-2219722;
                                                                                                                                                                                                                                                                                  01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last seq
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PIR; 142517; 142517.
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Best Local Similarity 32.0.
                                                                                                                      Local Similarity 32.0
                                                                                                                                                                                                                                                         STANDARD;
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NCBI_TaxID=10249;
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ETF2_VACCT
ID ETF2_VACCT
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P20635;
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Matches
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-!- FUNCTION: ACTS WITH RNA POLYMERASE TO INITIATE TRANSCRIPTION FROM EARLY GENE PROMOTERS. A DNA-DEPENDENT ATPASE ACTIVITY IS ASSOCIATED WITH VETF.
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                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jin Q., Hou Y.D., Cheng N.H., Yao E.M., Cheng S.X., Yang X.K., Jing D.Y., Yu W.H., Yuan J.S., Ma X.J.; "Complete gehomic sequence of vaccinia virus (Tian Tan strain)."; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Early transcription factor 82 kDa subunit (VETF large subunit).
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 710;
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SEQUENCE 710 AA; 82290 MW; 8C19BE5C578C5361 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB 1;
Pred. No. 77;
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7; Mismatches
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Best Local Similarity 32...
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                                                                                                                                                                                                                                                                                                                                                                                 Vaccinia virus
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Search completed: July 8, 2003, 16:25:05 Job time: 11.2564 secs

1 EKAP-----AHLSLPDPQALKRDV 19
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33 EKSPIYYFLRSHLNIQQPEIVKRHI 57

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 8, 2003, 16:17:10; Search time 40.9231 Seconds (without alignments) 95.665 Million cell updates/sec Run on:

US-09-824-647-6 98 1 EKAPAHLSLPDPQALKRDV 19 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 seqs, 206047115 residues Searched: 671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

sp_vertebrate:*
sp_unclassified:* sp_invertebrate:* sp_mammal:* sp_rvirus:*
sp_bacteriap:*
sp_archeap:* sp_organelle: SPTREMBL_21:* : sp_archea:* : sp_bacteria:* sp_rodent:* sp_plant:* sp_virus:* sp_human:* sp_fungi:* sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	99h8s1 homo sapien	09d2v3 mus musculu	ugr0 homo sapien	2786 acinetobact	29h9d1 homo sapien	19nvp9 homo sapien	wx33 homo sapien	Q8vel6 mus musculu	0949x8 arabidopsis	9lex9 arabidopsis	19c8a6 arabidopsis	28rv12 arabidopsis	092p26 rhizobium m	8tks0 methanosarc	Q55654 synechocyst	093341 struthio ca
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æ	Ouery Match	100.0	51.0	50.0	48.0	48.0	48.0	48.0	46.9	46.9	46.9	46.9	46.9	45.9	45.9	45.9	45.4
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133 13	13 16 17	1000	119 119 119 119	14 E S S 3 A 5 1 1 6 1 1 9 1 1 9 1 1 9 1 1 9 1 1 9 1 1 9 1 1 9 1 1 9 1 1 9 1 1 9 1 1 9 1 1 9 1 1 9 1 1 9 1 1 9 1 1 9 1 1 9 1 9 1 1 9 1
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ALIGNMENTS

1 EKAPAHLSLPDPQALKRDV 19

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MEDLINE-99265973; PubMed-10331946;
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Pfam; PF00536; SAM; 1.
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   NCBI_TaxID=9606;
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MEDLINE-21085660; PubMed-11217851;

MEDLINE-21085660; PubMed-11217851;

MEDLINE-21085660; PubMed-11217851;

MEDLINE-21085660; PubMed-11217851;

MARAWA T., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishli Y.,

Arakawa T., Sara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Alzawa K., Izawa M., Nishl K., Kiyosawa H., Kondo S., Yamanaka I.,

MA Alzawa K., Izawa M., Nishl K., Moobori T., Bono H., Kasukawa T., Saito R.,

MA Alzawa K., Ashburner M., Batalov S., Casavant T.,

MA Radota K., Matsuda H.A., Staubi F., Tomita M., Wagner I., Washio T.,

Sakai K., Okido T., Euruno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Bromstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M.,

My Cusnincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Sullaria Y., Storch K.-F.,

Nyashaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki.S.,

Masahizaki Y.,

Mayahizaki Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAY-2000 (TremBirel. 13, Created)
01-WAY-2000 (TremBirel. 13, Last sequence update)
01-JUN-2002 (TremBirel. 21, Last annotation update)
SCML2 protein (DJ1129A6.1) (sex comb on midleg (Drosophila)-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Adult male kidney CDNA, RIKEN full-length enriched library,
clone:0610012H06, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 50; DB 11; Length 589; Pred. No. 8.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00799; GRANULINS; 7.
PS00118; PA2_HIS; UNKNOWN_1.
589 AA; 63405 MW; 1DE8229C413CA292 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             700 AA.
                                                                                                                                                            589 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AK018744; BAB31384.1; -.
MGD; MGI:95832; Grn.
InterPro; IPR000118; Granulin.
InterPro; IRR01211; PhospholipaseA2.
Pfam; PF00396; granulin; 7.
SWART; SM00277; GRAN; 7.
                                                                                                                                                                                                                          Created)
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                                                                                                                                                            PRT;
   166 EKAPAHLSLPDPQALKRDV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EKAPAHLSLPDPQALKRD 18
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 61.1
Matches 11; Conservative
                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    01-JUN-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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0900R0
1D 0900
AC 0900
DT 01-M
DT 01-M
DT 01-S
DE 2)...
GN SCML
OS BURG
                                                                                           RESULT 2
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Gaps
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Montini E., Buchner G., Spalluto C., Andolfi G., Caruso A., de Dunnen, J.T., Trump D., Rocchi M., Ballabio A., Franco B.; aldentification of Schill, a Second Human Gene Homologous to the Drosophila Sex comb on midleg (Scm): a New Gene Cluster on Mp22.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 700;
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                                                                                                                                                                                                                                Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00454; SAM; 1.
SEQUENCE 700 AA; 77256 MW; 05E086D4928DEE73 CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 18.4 kba protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acinétobacter haemolyticus.";
Eur. J. Blochem. 254404412(1998).
EMBL: 256927; CAB09655.1;
-Interpro: IPR002106; AATRIN.LIGASEII.
PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 50.0%; Score 49; DB 4; Best Local Similarity 43.8%; Pred. No. 15; Matches 7; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 AA.
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01-MAR-2001 (TrEMBLrel. 16, Created)
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EMBL; AL096763; CAB65926.1; -.
                                                                                                                                                                        SEQUENCE OF, 245-700 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        607 EAPSYIAVPDPSVLKQ 622
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                                                                                                                Genomics 58:65-72(1999).
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                                                                                                                                                                                                                                                                                                                InterPro; IPR004092; Mb
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Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
DNA Res. 5:169-176(1998).
                                                                                                                                                                                                                                                                                                                         Match
Local Similarity 52.9%; Pred. No. 44;
Local Similarity 52.9%; Pred. No. 44;
Local Similarity 52.9%; Pred. No. 44;
Local Similarity 54; Mismatches 64; Indels
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                           Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                              915 AA; 104041 MW; 3CAC94C174C9A677 CRC64;
                                                                                                                                         MEDLINE-98403880; PubMed-9734811;
                                                                                                                                                                                                                                                  EMBL; AL159997; CAD13341.1; -. EMBL; AB014525; BAA31600.1; -.
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                                                                                                          SEQUENCE OF 125-915 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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                                              SEQUENCE FROM N.A.
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EMBL; AKO01456; BAA91701.1; S. CAC902297F0EA129 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                               Euteleostomi;
Homo.
                                                                                                                                                         Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Magai K., Sugano S., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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   01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
CDNA FLJ12840 fis, clone NT2RP2003277, weakly similar to NAM7
                                                                                                                                                                                                                                                                                                               Score 47; DB 4; Length 324;
Pred. No. 14;
2; Mismatchės 6; Indels
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                                                                                                                                                                                                                                   "NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ARC02902; BABLA299.1;
SEQUENCE 324 AA; 35932 WW; EDBEA2D23EC145F4 CRC64;
                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, F
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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Last annotation update)
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Last annotation update)
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BA479K20.2 OR KIAA0625.
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01-WAR-2002 (TrEMBLrel. 20, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TIEMBLREN: 15, Created)
01-OCT-2000 (TIEMBLREN: 15, Last seq
01-DEC-2001 (TIEMBLREN: 19, Last ann
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175 ERPPVHDQLQDPRLLKR 191
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                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 52.9%;
Matches 9; Conservative
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                                                                Homo sapiens (Human)
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Matches 9; Conserv
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                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                               NCBI_TaxID=9606;
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Gaps

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Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC018234; AAH18234.1; -.
                                                                                                                                                                                                                                                                                                                                                                               NON_TER 1 1 1 SEQUENCE 174 AA; 20018 MW; 75250AD38F86A088 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Putative n-calpain-1 large subunit (Fragment).
                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 46; DB 11;
Pred. No. 10;
  174 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                      01-WAR-2002 (TIEMBLrel. 20, Last sequenc
01-WAR-2002 (TIEMBLrel. 20, Last annotat
Hypothetical 20.0 kba protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
                                                  Created)
  PRT;
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QBVEL6 PRELIMINARY;
QBVEL6;
01-MAR-2002 (TrEMBLrel. 20,
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SEQUENCE

Q9LEX9 RESULT 10 Q9LEX9

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 1130712;

MICLINE-21016719;

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Theologis A., Care J.R., Palm C.J., Federspiel N.A., Kaul S.,

Mite O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Bunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Full C.Y.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

A chung M.K., Conline T.V., Feng J.-D., Fong B., Fulli C.Y.,

A chung M.K., Colkanish J., Johnson-Hopson C., Khan S., Khaykin E.,

Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Lin X., Liu S.X., Liu Z.A., Lee J.M., Naroney T., Rowley D.,

Aniltscher J., Miranda M., Nguyen M., Nlerman W.C., Osborne B.I.,

Pal G., Peterson J., Pham P.K., Rizzo M., Naroney T., Rowley D.,

Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sakano H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Wu D., Yu G., Fraser C. M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Calpain-like protein.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brasslcales; Brassicaceae; Arabidopsis.
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Lid S.E., Gruis D., Jung R., Lorentzen J.A., Ananiev E.,
Chamberlin M., Niu X., Meeley R., Nichols S., Olsen O.A.;
"The defective kernel 1 (dekl) gene required for aleurone cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46; DB 10; Length 21
Pred. No. 1.6e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00704; ĈALPAIN.
SMART; SM00230; CYSPC; 1.
PROSTIE; PS00139; THIOL, PROTENSE CYS; 1.
SEQUENCE 2143 AA; 236779 WW; B91A15081AF26EC2 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
N-calpain-1 large subunit, putative.
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EMBL, AC027034; AAG51565.1; -
InterPro; IPR001300; Protease_22.

InterPro; IPR000169; SHprot_acsite.

Pfam; PF01067; Calpain_III; 1.

Pfam; PF00648; Peptidase_22; 1.
                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear
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hes 8; Conservative
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                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-3702;
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Best Local S
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ID Q8RVL2
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                         Goldsmith A.D., Jiang P.K., Banh J., Banno F., Dale J.M.,
Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,
Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
Full Length cDNA of gene F7A10.23 (GI:12323169).";
Submitted (ANG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, ANG-0210, ANK.
SMART; SM00248; ANK: 1.
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Cholsne N., Robert C., Brottier P., Wincker P., Cattolico L.
Artiquenave F., Saurin W., Weissenbach J., Mewes H.W., Rudd
Lemoke K., Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 46; DB 10; Length 543;
Pred. No. 36;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.9%; Score 46; DB 10; Length 18
52.9%; Pred. No. 1.4e+02;
.ive 3; Mismatches 5; Indels
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
ENBL; A31389732; CAB94128.1; -.
InterPro; IRR000409; Beige_BEACH.
Pfam; PF02138; Beach; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    543 AA; 59467 MW; FB988FE03FD3AD48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 203.1 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 2143 AA.
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PNOSTYE; PS50197; BEACH; 1.
Hypothetical protein. 203121 MW;
SEQUENCE 1857 AA; 203121 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1336 EAPAHPAPPAPPERRD 1352
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Best Local Similarity 61.5%;
Matches 8; Conservative
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337 HLSITDPSAARRD 349
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Best Local Similarity 52.9
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANK repeat; Repeat.
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                                                                     SEQUENCE FROM N.A.
NCBI_TaxID=3702;
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Q9C8A6

RESULT 11 Q9C8A6

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Gaps

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Length 2143;

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Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P., FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A., Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R., Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W., Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M., Hedderich R., Ingram-Smith C., Kuetiner H.C., Krzycki J.A., Springer T.A., Umayam L.A., White O., White R.H., de Macario B.C., Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I., Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I., Metcalf W.W., Birren B., The genome of Methanosarcina acetivorans reveals extensive metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.9%; Score 45; DB 17; Length 299; 56.2%; Pred. No. 27; ive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Complete proteome.
SEQUENCE 299 AA; 32345 MW; 68006B7448C5F426 CRC64;
STRAIN=C2A / ATCC 35395 / DSM 2834;
MEDLINE-21929760; PubMed-11932238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and physiological diversity.";
Genome Res. 12:532-542(2002).
EMBL; AE011037; AAM06697.1; -.
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Best Local Similarity 56.27
Conservative
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Best Local Similarity
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Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
Godrie T., Goffeau A., Rahn D., Kiss E., Lelaure V., Masuy D.,
Godrie T., Goffeau A., Purnelle B., Ramsperger U.,
Renard C., Thebault P., Vandenbol M., Weidner S., Gallbert F.,
*Analysis of the chromosome sequence of the legume symbiont
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
EMBI, ALS91789; CAC46549.1;
InterPro; IPR000847; HTLLYSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
       development in the endosperm of maize grains encodes a membrane protein of the calpain gene superfamily."; Proc. Natl. Acad. Sci. U.S.A. 99:5460-5465(2002). EMBL; AY061803; AAL38186.1; SEQUENCE 2151 AA; 238262 MW; 50D571D7446A5609 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                      Score 46; DB 10; Length 2151;
Pred. No. 1.6e+02;
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Pred. No. 25;
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                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 AA; 30379 MW; B9F223D63CE788B7 CRC64;
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Last annotation update)
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Last annotation update)
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PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
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(TrEMBLrel. 21, I
(TrEMBLrel. 21, I
                                                                                                                                                                                                                      Query Match 46.9%;
Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein MA3328
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337 HLSITDPSAARRD 349
                                                                                                                                                                                                                                                                                                                                                                     6 HLSLPDPQALKRD 18
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241 ERAPAHLGLP 250
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SEQUENCE FROM N.A.
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01-JUN-2002 (
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Gaps

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Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugiura M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis Sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96127529; PubMed-8590279;
Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Complete proteome.
SEQUENCE 374 Aa; 42416 MW; 99D408A4D0BDA50F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NAR-2002 (TrEMBLrel. 20, Last annotation update) Hypothetical protein slr0358.
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Pred. No. 35;
                                                                                                                                                                                                    374 AA.
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01-NOV-1996 (TrEMBLrel. 01, Created)
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11 11 : : : : : 1 11 281 EKYPALFEVPEPQDLK 296
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0; Gaps

5; Indels

2; Mismatches 7; Conservative Matches

2 KAPAHLSLPDPQAL 15: :| || || || || : 339 RPPVHLDLPDPSKM 352

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Search completed: July 8, 2003, 16:28:02 Job time: 42.9231 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein July 8, 2003, 16:08:55; Search time 35 Seconds Run on:

(without alignments) 53.300 Million cell updates/sec

US-09-824-647-7 74 Title: Perfect score: Sequence:

1 ARRGTKCLRREAPR 14

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

908470 segs, 133250620 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

A_Geneseq_101002:* Database :

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:* /gcgdata/geneseq/geneseqp-emb1/AA1997.DAT: /SIDS2/gcgdata/geneseg/genesegp-embl/AA1985.DAT: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1986.DAT: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1987.DAT: /SIDS2/gcgdata/geneseg/genesegp-embl/AA1999 /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982. /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988 gcgdata/geneseq/genesegp-embl/AA198 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA199 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA199 /SIDS2/gcgdata/geneseq/genesegp-emb1/AA199 /SIDSZ/gcgdata/geneseg/genesegp-emb1/AA196 /SIDS2/gcgdata/geneseg/genesegp-emb1/AA196 /SIDS2/gcgdata/geneseg/genesegp-embl /SIDS2/gcgdata/geneseq/geneseqp-embl /SIDS2/gcgdata/geneseq/genesegp SIDS2, /SIDS2

RESULT 1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Ouerv				
No.	Score	Match	Match Length DB ID	DB	OI.	Description
-	74	100.0		20	AAW85481	Human GP88 autocri
7	74	100.0	•	14	AAR48673	Granulin sequence.
m	74	100.0		20	AAW85475	Human GP88 autocri
ಶ	74	100.0		23.		Human granulin/epi
S	9	91.9		22		Human protein sequ
9	68	91.9		12		Human epithelin pr
7	68	91.9		21	AAB43971	Human cancer assoc
80	53	71.6		20	AAW85479	Mouse GP88 autocri
6	53	71.6	583	12		Mouse epithelin pr
10	<u>23</u>	71.6		20	AAW85474	Mouse GP88 autocr1

Mouse granulin/epi Rat epithelin prec Propionibacterium Granulin E. Homo Amino acid sequenc Herbicidally activ	Zea mays protein f Profionibacterium Propionibacterium Propionibacterium Novel human diagno Flavobacterium ker Human nucleotide p	Mouse neuro-growth Murine protein iso Mouse TANGO 125 (T Mouse Tal25 (TANGO- MOUSE neuro-growth Mouse Notch4-like	Propionibacterium Propionibacterium Novel human neopia Novel human neopia HSV-2 strain SB5 C Novel human neopia	HSV-2 strain SBS C HSV-2 VP22 protein Novel human diagno Novel human diagno Human polypeptide Human macro protei
		<i>(</i> -	v _i	
AAE20520 AAR14325 AAU48409 AAR41885 AAY29199 ABB92875	AAG40966 AAU63381 AAU43048 AAU47116 ABG23868 AAW56275 AAW49674	AAW88397 ABB72368 AAY52141 AAE21081 AAW88392 AAE05356	AAU49368 AAU48478 AAU21798 AAW72069 AAU21670	AAW72214 AAW67755 ABG30299 ABG24248 AAM39448 AAM39447 ABB84252 ABG05609
23 14 20 20 23	70 70 70 70 70 70 70 70 70 70 70 70 70 7	53 53 53 53 53 53 53	222222	5355556
589 589 101 56 113	88 55 76 255 422 1156	255 275 275 278 278 278	99 70 119 131 137	302 306 621 655 737 761 761
71.6 68.9 62.2 58.1 55.4	54 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	522.7 522.7 522.7 522.7 522.7	52.0 51.12 51.12 51.4 5.14 5.14	511.6 511.8 511.8 51.1.8 51.1.8 7.1.8
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ALIGNMENTS

GP88; granulin; epithilin; human; growth factor; autocrine; tumour; cancer; viral infection; antagonist; therapy; diagnosis; antigen; antibody. Human GP88 autocrine growth factor antigenic peptide Al4R. AAW85481 standard; Peptide; 14 AA. 15-MAR-1999 (first entry) AAW85481;

Homo sapiens.

WO9852607-A1.

98WO-US10555. 22-MAY-1998; 26-NOV-1998.

97US-0991862 97US-0863079 16-DEC-1997; 23-MAY-1997;

Serrero G;

(SERR/) SERRERO G.

WPI; 1999-045276/04.

Composition containing antagonist of growth factor GP88 - useful for treating cancer and viral diseases and also for diagnosing disease

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593 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            (SERR/) SERRERO G.
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                                                                                                                                                                                                                                                                                                                                                                                        22-MAY-1998;
                                                                                                                                                                                                                                                            Homo sapiens
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23-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                             AAW85475;
 Sequence
                    Query Match
                                                                                                                                                                                                                                                                                  Key
Peptide
                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                 RESULT 3
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                                                                       tightly regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which acts as a stringently required growth stimulator for the tumorigenic cells. Al4R was used in an attempt to raise neutralising antibodies to GP88 (see also AAW85480). Antagonists to GP88, such as anti-GP88 antibodies, are used to treat diseases associated with increased expression of GP88, particularly cancer but also viral infections. Anti-GP88 antibodies can also be used
                                                    is an 88
                                                                                                                                                            diagnostic reagents and to deliver toxins or other compounds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The granulin inhibits keratinocytes and is useful in formulations for promoting the healing of wounds.
                                                                                                                                                                                                                                       ö
                                         This is the amino acid sequence of peptide A14R, comprising am acid residues A566-R579 of human GP88 (see AAW85475). GP88 is kDa glycoprotein autocrine growth factor that is expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New cystine rich granulin peptide(s) from leucocyte(s) - are keratinocyte inhibitors useful topically for wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                       Granulin; keratinocytes; wound healing; inhibition; peptide; granulocytes; leucocytes.
                                                                                                                                                                                                              100.0%; Score 74; DB 20; Length 14; 100.0%; Pred. No. 3.5e-06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Glycine encoded by CAG."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note- "Valine encoded by ATG."
539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
452
                                                                                                                                                                                                                                                                                                                                    AAR48673 standard; Protein; 593 AA.
                      Page 45; 86pp; English.
from altered GP88 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92WO-CA00089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92US-0829233
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                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                     14; Conservative
                                                                                                                                                                       GP88-expressing cells
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                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   Granulin sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SOLO/) SOLOMON S.
                                                                                                                                                                                            14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ49052.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9315195-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-AUG-1993,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Solomon S;
                                                                                                                                                                                                                                                                                                                                                           AAR48673;
                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                              RESULT 2
AAR48673
ID AAR4
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                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition containing antagonist of growth factor GP88 - useful for treating cancer and viral diseases and also for diagnosing disease from altered GP88 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GP88; granulin; epithilin; human; growth factor; autocrine; tumour; cancer; viral infection; antagonist; therapy; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
340..364
/note= "El9V peptide used to raise antibody"
/note= "A14R peptide used to raise antibody"
Length 593;
                                                   Indels
   DB 14;
0.00013;
thes 0;
                                                                    Mismatches
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   Score 74;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                        AAW85475 standard; Protein; 593 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human GP88 autbcrine growth factor.
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      100.0%;
100.0%;
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970S-0863079.
                                                                                                                                                                     1 ARRGIKCLRREAPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAR-1999 (first entry)
                                   Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           granulin precursor; GP88; cytostatic; tumourigenicity; tamoxifen; pplastic; antioestrogen therapy; skin cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diagnosing tumorigenicity in a human, comprising obtaining a cell sample, detecting GP88 in the cells, and determining the number of GP88 positive cells in the sample -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method for diagnosing tumourigenicity in a
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346..364
/note= "Region used as antigen to develop anti-human
GP88 neutralising antibody"
                                                              ó
     Length 593;
                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human granulin/epithelin precursor (GP88) protein.
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     Score 74; DB 20;
Pred. No. 0.00013;
                                                           0; Mismatches
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     100.0%;
100.0%;
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                                                                                                                                             566 ARRGIKCLRREAPR 579
                                                                                                              1 ARRGIKCLRREAPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
Ouery Match 100.
Best Local Similarity 100.
Matches 14; Conservative
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N-PSDB; AAD32850.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SERR/) SERRERO G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             593 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antineoplastic;
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08-DEC-1999;
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                                                                                                                                                                                                                                                   RESULT
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full-length CDNAs defined in the specification. Where a primer set full-length CDNAs defined in the specification. Where a primer set comprises: (a) an oligor-off primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 1'-end sequence complementary to a oligonucleotide comprises at 1'-end sequence complementary to a constitute 5'-end sequence/3'-end sequence is selected from three antimer of the 5'-end sequence is selected from three antimer of the sequence is selected from three antimers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length conner. The primers are also useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                            Human; primer; detection; diagnosis; antisense therapy; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
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Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; SEQ ID 15310; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                              Human protein sequence SEQ ID NO:15310.
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                                                                                                                 AAB94550 standard; Protein; 413 AA.
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T, Wakamatsu
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2000JP-0183767.
S66 ARRGTKCLRREAPR 579
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                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                413 AA;
                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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11-JAN-2000;
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                                                                                                                                                                                             26-JUN-200F
                                                                                                                                                          AAB94550;
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                                                                              RESULT 5
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Query Match

Score 74; DB 23; Length 593; Pred. No. 0.00013;

100.0%; 100.0%;

Best Local Similarity

Query Match

NAME OF THE PART O

Gaps

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AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB4339 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidabetic; antiasthmatic; antihheumatic; antibarterial; antihihyroid; antihalleragic; antibarterial; antihityroid; antihalleragic; antibacterial; antihiral; dermatological; neuroprotective; cardiant; thrombolytic; coaquiant; nootropic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dermatological; neuroprotective; thrombolytic; coaquiant; notropic; vasotropic; antipsorlatic; antiangiogenic; gene therapy; inflammation; immune disorder; heratological disorder; autoimmune disorder; altoimmune disorder; heration; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
bioactivity. In contrast, however, ET-2 is apparently not capable of eliciting the growth stimulatory activity characteristic of ET-1 and, in fact, antagonises this ET-1 activity.

See also ARO14338-40, ARO14952-53, AAR14328-9 and AAR15315-20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer -
                                                                                                                                                                                Score 68; DB 12; Length 593; Pred. No. 0.0015; Mismatches 1; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cancer associated protein sequence SEQ ID NO:1416.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB43971 standard; Protein; 621 AA.
                                                                                                                                                                              91.9%;
Local Similarity 92.9%;
hes 13; Conservative (
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                                                                                                                                                                                                                                                                                                                              1 ARRGTKCLRREAPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                       593 AA;
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                                                                                                                                       Sequence
                                                                                                                                                                                            Query Match
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Matches
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                                 ö
                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epithelins - useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New cysteine-rich growth modulating proteins, epithelins - us as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis
                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ET; growth regulation; inhibition; stimulation.
     Pred. No. 0.001;
0; Mismatches
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/note= "claim 8, page 55"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label EP-2
/note "claim 3, page 53"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "claim 4, page 53"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              label- precursor
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/note= "claim 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note- "claim 2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BRIM ) BRISTOL-MYERS SQUIB.
     92.98;
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90US-0504508
                                                                                                              386 AARGTKCLRREAPR 399
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                                                                                     1 ARRGTKCLRREAPR 14
                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human epithelin precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     282..337
/label- E
     Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shoyab M, Plowman GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1991-325168/44.
N-PSDB; AAQ14339.
                                                                                                                                                                                                                                                                                                                                                                               17-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-APR-1991;
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03-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9115510-A.
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                                                                                                                                                                                                                                                                                                                              AAR14326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
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                                                                                                                                                                                                                    RESULT 6
AAR14326
ID AARX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
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Gaps

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Indels

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Mismatches

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label- EP
                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      label- EP
                                                                                                                                                                                                                                Mouse epithelin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .570
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                                                                                                                                                                                                                                                                                                                                                                                                                             .261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .416
         9; Conservative
                                   RGTKCLRREAPR 14
                                                    Shoyab M, Plowman GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VPI; 1991-325168/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAQ14340
                                                                                                                                                                                                                                                                                           Mus musculus;
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03-APR-1990;
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                                                                                                                                                                                                  17-JAN-1992
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                                                                                                                                                                       AAR14327;
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         Matches
                                                                                                             RESULT 9
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disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and absterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the amino acid sequence of peptide S14R, comprising amino acid residues S562-R575 of murine GP88 (see AAW85474). GP88 is an 88 kDa glycoprotein autocrine growth factor that is expressed in a tightly requiated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which acts as a stringently required growth stimulator for the tumorigenic cells. S14R was used to raise neutralising antibodies to GP88. Antagonists to GP88, such as anti-GP88 antibodies, are used to treat diseases associated with increased expression of
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition containing antagonist of growth factor GP88 - useful for treating cancer and viral diseases and also for diagnosing disease from altered GP88 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibodies can also be used as diagnostic reagents and to deliver toxins or other compounds to GPB8-expressing cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                           GP88; granulin; epithilin; mouse; growth factor; autocrine; tumou
cancer; viral infection; antagonist; therapy; diagnosis; antigen;
                                                                                                                                                                                        ö
                                                                                                                                                       Score 68; DB 21; Length 621;
Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                Mouse GP88 autocrine growth factor antigenic peptide S14R.
                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    particularly cancer but also viral infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 53; DB 20;
Pred. No. 0.016;
                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                       AAW85479 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 8; Page 45; 86pp; English.
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75.0%;
                                                                                                                                                      / Match 91.9%;
Local Similarity 92.9%;
nes 13; Conservative
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                                                                                                                                                                                                                                   1 ARRGIKCLRREAPR 14
                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Best Local Similarity
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                                                                                                                           621 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SERR/) SERRERO
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                                                                                                                                                                                                                                                                                                                                                                                 15-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serrero G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                    AAW85479;
                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody
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Matches
                                                                                                                                                                                                                                                                                         RESULT 8
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ET-1 is a bifunctional growth regulator, capable of stimulating the growth of some call types while inhibiting the growth of others. ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory bloactivity. In contrast, however, ET-2 is apparently not capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                             New cysteine-rich growth modulating proteins, epithelins - useful as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis
                                                               sT; growth regulation; inhibition; stimulation.
                                                                                                                                                                                                       page 55"
                                                                                                                                                                                                                                                         page 56"
                                                                                                                                                                                                                                                                                 page 56"
                                                                                                                                                                                                                                                                                                          28, page 56"
                                                                                                                                                     52
                                                                                                                                                                             page 55
                                                                                                                                                                                                                               page 55
                                                                                                                           page 55'
                                                                                                       1, 589
/label= precursor
----- claim 21, F
                                                                                                  Location/Qualiflers
AAR14327 standard; Protein; 589 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 23; 97pp; English.
                                                                                                                                                                              23,
                                                                                                                                                                                                      claim 24,
                                                                                                                                                     22,
                                                                                                                                                                                                                               "claim 25,
                                                                                                                                                                                                                                                        "claim 26,
                                                                                                                                                                                                                                                                         'label= EP
'note= "claim 27,
                                                                                                                                                                                                                                                                                                  /label= EP
/note= "claim
                                                                                                                                            /label= EP-1
/note= "claim
                                                                                                                                                                             "claim
                                                                                                                                                                       label= EP-2
                                                                                                                                                                                                                                                                                                                                                                            910S-0083796.
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The invention relates to a method for diagnosing tumourigenicity in
                                                                                                                                                                                                                                                                                                                                                                                           Mouse; granulin
antineoplastic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
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                                                                                                                                                                                                                                                                                                                                           01-JUL-2002
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08-DEC-1999;
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                                                                                                                                   Sequence
                                                                                                                                                                                                                               564
                                                                                                                                                                                                                                                                                                                     AAE20520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
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                                                                                                                                                                                                                                                                    RESULT 11
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eliciting the growth stimulatory activity characteristic of ET-1 and in fact, antagonises this ET-1 activity.
See also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20.
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Composition containing antagonist of growth factor GP88 - useful for treating cancer and viral diseases and also for diagnosing disease from altered GP88 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is the amino acid sequence of murine GP88, an 88 kba glycoprotein autocrine growth factor and epithilin/granulin precursor that is expressed in a tightly regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which acts as a stringently required growth stimulator for the tumorigenic cells. Inhibition of GP88 expression or action in the tumorigenic cells results in an
                                                                                                                                                                                                                                                                                                         autocrine; tumour;
                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "K19T peptide, used to raise antibody"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to raise antibody"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               "P12T peptide used to raise antibody"
                                                                       Length 589
                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                      GP88; granulin; epithilin; mouse; growth factor; autocr:
cancer; viral infection; antagonist; therapy; diagnosis
                                                                       12;
                                                                                 0.6;
                                                                      Score 53; DB
Pred. No. 0.6;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 562..575
/note= "S14R peptide, used
                                                                                                                                                                                                                                                                                                                                                                                                                note- "encoded by AGC"
                                                                                                                                                                                                                                                                                                                                                                                         note- "encoded by CTG"
                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "encoded by TGA"
                                                                                                                                                                                                                                                                               Mouse GP88 autocrine growth factor.
                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                      AAW85474 standard; Protein; 589 AA.
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                                                                       71.6%;
75.0%;
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970S-0863079.
                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                 564 RGTKCLRKKIPR 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..362
                                                                                               9; Conservative
                                                                                                                    3 RGTKCLRREAPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                    208..219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note=
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N-PSDB; AAV82824.
                                                                     Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SERR/) SERRERO G.
                                               589 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
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23-MAY-1997;
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                                                                                                                                                                                                                               AAW85474;
                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
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                                                                                                                                                                                                                                                                                                                                             Mus sp.
                                                                                                                                                                                 RESULT 10
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precursor; GP88; cytostatic; tumourigenicity; tamoxifen; antioestrogen therapy; skin cancer.
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inhibition of the tumorigenic properties of the overproducing cells. Murine GP88 cDNA (see AAV82824) was obtained from the highly tumorigenic PC cell line. Antagonists to GP88 are used to treat diseases associated with increased expression of GP88, particularly cancer but also viral infections. Fragments of GP88 are used to raise specific antibodies (used as antagonists, as diagnostic reagents and for delivering toxins or other compounds to GP88 expressing cells) and to screen for antibodies. Methods are provided for diagnosing disease, or determining susceptibility to disease, resulting from altered GP88 activity.
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     344..362
/note= "Regions used as antigens to raise anti-GP88
antibodies"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Regions used as antigens to raise anti-GP88
antibodies"
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                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                          DB 20; Length 589;
0.6;
                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse granulin/epithelin precursor (GP88) protein.
                                                                                                                                                                                                                                                                                                                                  Score 53; DB 2
Pred. No. 0.6;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label- Unknown
/note- "Encoded by ATG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note- "Encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE20520 standard; Protein; 589 AA.
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                                                                                                                                                                                                                                                                                                                                          71.6%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2001; 2001US-0880842
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990S-0456886
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 75.uv.,
Best Local Similarity 75.uv.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 RGTKCLRŘEAPR 14
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N-PSDB; AAD32849.
                                                                                                                                                                                                                                                                                       589 AA;
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900S-0504508

03-APR-1990;

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human. The method comprises obtaining a biological sample containing cells from the patient, detecting GP88 in the cells of the sample, and determining the number of GP88 positive cells in the sample, and determining the ratio of GP88 positive cells to the total number of cells in the sample. The invention also relates to a method for determining in the sample. The invention also relates to a method for determining antioestrogen therapy. The method is useful for diagnosing tumourigenicity in a sample, such as blood, serum, plasma, urine, nipple aspirate, cerebrospinal fluid, liver, kidney, breast, bone, brain, lung, collon, or skin cancer. The method can be used to treat or prevent re-occurrence of cancer in a patient, by administering tamoxifen if the sample contains less than 10 % GP88, or less than 5 % GP88 positive
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                          ö
                                                                                                                                                                                                   Length 589;
                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                  Score 53; DB 23;
Pred. No. 0.6;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                             ET; growth regulation; inhibition; stimulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Noc.
280.335
/label- EP-1
.... "claim 12, page 54"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label- EP
/note- "claim 14, page 54"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= EP
/note= "claim 15, page 54"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     page 54"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       page 54"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "claim 13, page 54"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "claim 18, page 55"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1..589
                                                                                                                                                                                                                                                                                                                                 AAR14325 standard; Protein; 589 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "claim 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note- "claim 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note- "claim 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= precursor
                                                                                                                                                                                                   71.6%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      910S-0083796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label- EP
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                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                             Local Similarity 75.0 tes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205..261
/label= E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  570
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                                                                                                                                                                                                                                               3 RGTKCLRREAPR 14
                                                                                                                                                                                                                                                                                                                                                                                                      Rat epithelin precursor.
                                                                                                                                                                            589 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 409115510-A.
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                                                                                                                                                                                                                                                                                                                                                                              17-JAN-1992
                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                       AAR14325;
                                                                                                                                                                                                   Query Match
                                                                                                                                                      protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
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Matches
                                                                                                                                                                                                                                                                                                           RESULT 12
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SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                        ET-1 is a bifunctional growth regulator, capable of stimulating the growth of some cell types while inhibiting the growth of others. ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory bloactivity. In contrast, however, ET-2 is apparently not capable of eliciting the growth stimulatory activity characteristic of ET-1 and, in fact, antagonises this ET-1 activity. See also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20.
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                        epithelins - useful
                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                         New cysteine-rich growth modulating proteins, epithelins - us as inhibitors of neoplastic cell growth and to promote wound
                                                                                                                                                                                                                                                                                                                                                  Length 589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bhatia A;
                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes immunogenic protein #9305.
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Carter D;
                                                                                                                                                                                                                                                                                                                                                   Score 51; DB 12;
Pred. No. 1.3;
3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skeiky YAW, Persing DH, Mitcham JL,
T'maisonneuve J, Zhang Y, Jen S, Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU48409 standard; Protein; 101 AA
                                                                                                                                                                                 Disclosure; Fig 18; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                   68.9%;
66.7%;
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                           (BRIM ) BRISTOL-MYERS SQUIB.
                                                                                                                                                     healing and treat psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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564 KGTKCLRKKTPR 575
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                                                                                                                                                                                                                                                                                                                                                                                                             3 RGTKCLRREAPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Propionibacterium acnes
                                                       Plowman GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-616774/71.
                                                                                                                                                                                                                                                                                                                                      WPI; 1991-325168/44.
N-PSDB; AAQ14338.
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                                                                                                                                                                                                                                                                                                                         589 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200181581-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-FEB-2002
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                                                       Shoyab M,
                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU48409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
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25-OCT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                            AAY29199;
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                                                    Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by D. acnes. The disorders include SABHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The colypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies and downregulate expression and activity of P. acnes polypeptides and place and plac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The granulin inhibits keratinocytes and is useful in formulations for promoting the healing of wounds. This peptide was designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Granulin; keratinocytes; wound healing; inhibition; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 46; DB 22; Length 101;
Pred. No. 1.8;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New cystine rich granulin peptide(s) from leucocyte(s) – an
keratinocyte inhibitors useful topically for wound healing
Example 1; SEQ ID No 9604; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR41885 standard; peptide; 56 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 33; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.2%;
ilarity 64.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92WO-CA00089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | | | : | | | | | | ARRGSSCEGRERPR 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ARRGIKCLRREAPR 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     API; 1993-320328/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               granulin E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR41885;
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                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note: the sequences given in the specification were poorly legible, in some instances assumptions were made as to the identity of the residue; it is therefore possible that the sequence given below is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mahajan-Miklos S;
                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a virulence factor encoded by ORF26757c.
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Pred. No. 15;
2; Mismatches 3; Indels
  DB 14; Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virulence factors useful in developing disease treatments
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human pathogen; virulence polypeptide; virulence factor; pathogenic infection; Pseudomonas aeruginosa infection.
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                                                 Mismatches
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Job time : 36 secs
                                                                                                                                                                                                                                                                AAY29199 standard; Protein; 113 AA.
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58.1%;
100.0%;
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Tan M, Tsongalis
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RRGPRCIRRCARR 106
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                                               Conservative
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                                                                                                                          ARRGIKCL 56
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Best Local Similarity
'...hos 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-357851/30.
                                                                                                 1 ARRGIKCL 8
Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-NOV-1997;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                         OM protein - protein search, using sw model
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July 8, 2003, 16:21:00; Search time 8.61539 Seconds (without alignments) 47.812 Million cell updates/sec Run on:

US-09-824-647-7 74 Title: Perfect score: Sequence:

1 ARRGIKCLRREAPR 14

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

262574 seqs, 29422922 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep/cgn2_6/ptodata/1/iaa/backfiles1.pep ptodata/1/laa/5B_COMB.pep: /ptodata/1/laa/6A_COMB.pep: /cgn2_6/ptodata/1/laa/5A_COMB.pep Issued_Patents_AA:* /cdn2_6/ Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Query

Result

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Description	Sequence 7, Appli	Sequence 17, Appl	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 5, Appl1	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 2, Appli	ý	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 307, App	'n	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 52, Appl	Sequence 28, Appl	Sequence 24, Appl	Sequence 11, Appl	Sequence 7, Appli
<u> </u>																											
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er er	US-08-991-862-7	US-08-991-862-17	US-07-668-648-4	US-08-429-998-4	US-08-431-333-4	PCT-US91-02321-4	US-08-991-862-5	US-07-668-648-6	US-08-429-998-6	US-08-431-333-6	US-08-991-862-2	PCT-US91-02321-6	US-07-668-648-2	US-08-429-998-2	US-08-431-333-2	PCT-US91-02321-2	US-09-199-637A-307	US-09-230-421-2	US-08-712-072C-2	US-08-996-083-1	US-09-429-516-1	US-09-429-516-3	US-09-724-864-52	US-09-171-461-28	US-09-697-367-24	US-08-429-054A-11	US-08-718-777-7
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ength	14	593	593	593	593	593	14	589	589	589	589	589	589	589	289	589	113	301	422	1156	1156	1156	278	1121	368	1068	1068
Match Length DB	100.0	100.0	91.9	91.9	91.9	91.9	71.6	71.6	71.6	71.6	71.6	71.6	6.89	6.89	68.8	68.9	55.4	55.4	54.1	54.1	54.1	54.1	52.7	52.7	51.4	51.4	51.4
Score	74	74	68	99	99	68	53	53	53	53	. 53	53	51	51	51	51	41	41	40	40	40	40	39	39	38	38	38
No.	7	73	ო	4	ιń	9	7	80	6	10	11	12	13	14	15	16	17	18	13	20	21	22	23	24	25	56	. 27

THE OF INVENTION: GINETCE
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTACONISTS
FILE REPERENCE: 29996-488/7001-A
CURRENT APPLICATION NUMBER: US/08/991,862
CURRENT FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/863,862
EARLIER APPLICATION NUMBER: 09/65-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VOY: 2.0

Sequence 17, Application US/08991862 Patent No. 6309826 GENERAL INFORMATION:

US-08-991-862-17

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Gaps
APTICANT: SOLICAN: 3 S
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OTHER INFORMATION: Internal peptide of human GP88 used to develop

OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
US-08-991-862-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 74; DB 4; Length 14; Best Local Similarity 100.0%; Pred. No. 1e-06; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ARRGIKCLRREAPR 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 7
LENGTH: 14
TYPE: PRT
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FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
CORRESPONDENCE ADDRESS:
                                                                                                   COUNTRY: USA
ZIP: 10036
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                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/07668648
Patent No. 5416192
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Showman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                       Query Match 100.0%; Score 74; DB 4; Length 593; Best Local Similarity 100.0%; Pred. No. 4.3e-05; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOVEL CYSTEINE-RICH GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
URREWY APPLICATION DATA:
APPLICATION NUMBER: US/07/668,648
FILING DATE: 19910819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.9%; Score 68; DB 92.9%; Pred. No. 0.00 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REPERSUCK/DOCKEY UNMBER: 5624-161-999
FELECOMMUNICATION INFORMATION:
TELEPHONE: (212)/790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Pennie & Edmonds
1155 Avenue of the Americas
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; Patent No. 5885961

GENERAL INFORMATION:

APPLICANT: Shoyab, Mohammed

APPLICANT: Plowman, Gregory D.

TITLE OF INVENTION: EPITHELINS: NO

; TITLE OF INVENTION: MODULATING PRO

NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                   11111111111111
566 ARRGTKCLRREAPR 579
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AMINO ACID
                                                                                                                                                              1 ARRGTKCLRREAPR 14
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 91.9
Best Local Similarity 92.9
Matches 13; Conservative
                  ; ORGANISM: Human GP88 cDNA
US-08-991-862-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein US-07-668-648-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-429-998-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
TYPE: PRT
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Gaps
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GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
"TOTE OF INVENTION: ANDULATING PROFEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 593;
                                                                                                                                                          SOFTWARE:
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,998
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 68; DB 2; I
Pred. No. 0.00046;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                     REGISTRATION WUMBER: 18,872
REFERENCE/DOCKET\ NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITT: New York
STATE: New York
COUNTRY: USA
: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
                                                                                                                        COMPUTER: IBM PC compatible
OPERATING (SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08431333 Patent No. 5965723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: 1:-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 91.9%;
Best Local Similarity 92.9%;
Matches 13; Conservative
                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                        Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ARRGIKCLRREAPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-08-429-998-4
                                      New York
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Sequence 5, Application US/08991862
Patent No. 6309826
                                                                                                                                                                                                                                                                                                                                                                                                                                            71.6%;
75.0%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 RGTKCLRREAPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 RGTKCLRKKIPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: EPITILE OF INVENTION: MOI NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: mouse granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 9; Conserv
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: USA
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-668-648-6
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Sequence 4, Applications
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TILE OF INFURION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TILE OF INFURION: MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 68; DB 5; Length 593;
Pred. No. 0.00046;
                                                                                                                                                                                                                                            Length 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02321
FILING DATE: 19910403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Bristol-Myers Squibb Company 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                 ed. No. 0.0
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOOKET NUMBER: ON0071A-PC
TELECOMMUNICATION INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 56.
TELECOMMUNICATION:
TELEPHONE: (212)790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.9%;
92.9%;
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Best Local Similarity 92.9%;
Matches 13; Conservative
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                                                               TELEPHONE: (212)799-9090
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 4-
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                    (206)728-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 593 amino acids TYPE: AMINO ACID
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                                                                                                                                        : 593 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                  1 ARRGTKCLRREAPR 14
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Best Local Similarity 92.99
"-+ches 13; Conservative
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                                                                                                                                                                    ; TOPOLOGY: linear;
; MOLECULE TYPE: protein
US-08-431-333-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein PCT-US91-02321-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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GENERAL INFORMATION:

APPLICANT: SETTETO, GINETLE

APPLICANT: SETTETO, GINETLE

TITLE OF INVENTION: 88 ADD TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS

FILE REPERRACE: 19996.488/P001.A

CURRENT APPLICATION NUMBER: 08/08/991,862

CURRENT FILING DATE: 1997-05-23

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PATENTIN VET: 2.0

SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1): (14)
OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the OTHER INFORMATION: antisera against the GP88 used in the CHER INFORMATION: immunoaffinity step.
US-08-991-805-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gregory D. EPITHELINS: NOVEL CYSTEINE-RICH GROWTH MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPOTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION UNDER: US/07/668,648
FILING DATE: 19910819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 53; DB 4;
Pred. No. 0.0043;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/07668648
Patent No. 5416192
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
MAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 5
TELECOMMUNICATION INFORMATION
TELEPHONE: (212)790-9090
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MOLECULE TYPE: protein

RESULT

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CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES:
                                                                                                                   10036
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US-08-991-862-2
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                                                                       Gaps
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                                                                                                                                                                                                                                                                              APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPITHELINS: NOVEL CYSTEINE-RICH GROWTH MODULATING PROTEINS
                                  DB 1; Length 589;
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                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/429,998
FILING DATE: 27-APR-1995
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US-08-431-333-6
; Sequence 6, Application US/08431333
; Patent No. 5965723
                                                                                                                                                                                                        US-08-429-998-6; Sequence 6, Application US/08429998; Patent No. 5885961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.6%;
75.0%;
                               Query Match 71.6%;
Best Local Similarity 75.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212)790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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564 RGTKCLRKKIPR 575
                                                                                                                         1111111:: 11
564 RGTKCLRKKIPR 575
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Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                      3 RGTKCLRREAPR 14
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                           New York
: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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us-07-668-648-6
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Gaps
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APPLICANT: SETECTO, GINETTE
TITLE DOF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
TITLE REFERENCE: 29996.488/PP001-A
CURRENT APPLICATION NUMBER: US/08/991,862
CURRENT FILING DATE: 1998-08-17
EARLIER PELLING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PETENTIN VET. 2.0
LENGTH: 589
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Pred. No. 0.18;
2; Mismatches 1; Indels
                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,333
FILING DATE: 27-APR-1995
CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                        5624-161-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 53;
ADDRESSEE: Pennie & Edmonds
STRET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No
                                                                                                                                                                                                                                                                                                                    UMBER: US 07/668,648
13-MAR-1991
                                                                                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Mouse epithelin/granulin
US-08-991-862-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08991862 Patent No. 6309826
                                                                                                                                     MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING CVCMPM.
                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 5(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.6%;
75.0%;
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75.0%;
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NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 869-9741 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              589 amino acids
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564 RGTKCLRKKIPR 575
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Best Local Similarity 75.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 13-MAR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear; MOLECULE TYPE: protein US-08-431-333-6
                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                            OPERATING, SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
GOMPOTER: IBM PC compatible
OOPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.39;
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                                                                                                                                                                                                                                                                                                                                                     Mismatches
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REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 51;
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR AFFICATION DATA:
PRIOR DATE:
RILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08429998
Patent No. 5885961
GENERAL INFORMATION:
                                              NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 56
                                                                                                       TELECOMMUNICATION INFORMATION
TELEPRONE: (212)790-9090
TELERAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.9%;
66.7%;
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TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 589 amino acids
                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 589 amino acids
TYPE: AMINO ACID
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Best Local Similarity 66.7
Matches 8; Conservative
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Best Local Similarity 66.7
Matches 8; Conservative
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19910819
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                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-07-668-648-2
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ADDRESSEE: Pennie &
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New York
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GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVERTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF TWENTION: MODULATING PROTEINS
                                                                       APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
UNMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 589;
                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02321
FILING DATE: 19910403
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                                                                                                                                                                                  E: Bristol-Myers Squibb Company 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,648
                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                  Sequence 6, Application PC/TUS9102321 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/07668648 Patent No. 5416192
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COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: POOL, Brian.W.
REGISTRATION NUMBER: 32,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: ON
TELECOMMUNICATION INFORMATION
TELEPHONE: (206)728-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 589 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 75.0
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564 RGTKCLRKKIPR 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
NEDIUM TYPE: Floppy
                                                                                                                                                                                                                     CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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RESULT 13

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APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA

2IP: 10036

ZIP: 10036

ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7%; Pred. No. 0..
Matches 8; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/431,333
FILING DATE: 27-APR-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
CONWYRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAME: MISTOCK, S. Legile
REGISTRATION NUMBER: 16,872
REFREENCE/POCKET NUMBER: 5624-
FELECOMMUNICATION INFORMATION:
FELEPHONE: (212)790-9090
FELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 589 amino acids
FIREST amino acids
FIREST HOPOLOGY: linear
MOLECULE TYPE: protein
US-08-431-333-2
                                                                                                                                                        Sequence 2, Application US/08431333
Patent No. 5965723
GENERAL INFORMATION:
                       :||||||||: ||
564 KGTKCLRKKTPR 575
3 RGTKCLRREAPR 14
                                                                                                                                   US-08-431-333-2
                                                                                                             RESULT 15
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Indels

Search completed: July 8, 2003, 16:30:21 Job time: 9.61539 secs

:|||||||::|| 564 KGTKCLRKKTPR 575 3 RGTKCLRREAPR 14

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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2003, 16:24:26; Search time 13.641 Seconds

(without alignments)
119.483 Million cell updates/sec
Title: US-09-824-647-7
Sequence: 1ARRGTKCLRREAPR 14
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 445758 seqs, 116419773 residues
Total number of hits satisfying chosen parameters: 445758
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database: Published_Applications_AA:*

Published_Applications_AA:*

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2: /cgn2_6/ptodata/2/pubpaa/DC07_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/DC06_PUBCOMB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/DC06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/DC06_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/DC08_PuBCOMB.pep:*

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9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

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12: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 7, Appli	Sequence 17, Appl	Sequence 1416, Ap	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appl1	Sequence 5, Appli	Sequence 2, Appli	Sequence 2, Appli	Segmence 2, Appli								
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	QI .	US-09-824-647-7	US-10-218-509-7	US-10-281-160-7	US-09-813-156-7	US-09-824-807-7	US-09-824-647-17	US-10-218-509-17	US-10-281-160-17	US-09-813-156-17	US-09-824-807-17	US-09-925-301-1416	US-09-824-647-5	US-10-218-509-5	US-10-281-160-5	US-09-813-156-5	US-09-824-807-5	US-09-824-647-2	US-10-218-509-2	US-10-281-160-2
	DB	6	σ	6	2	10	σ	6	6	7	2	10	σ	6	σ	7	ដ	6	σ	σ
	Query Match Length DB	14	14	14	14	14	593	593	593	593	593	621	14	14	14	14	14	589	589	589
фP	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	91.9	71.6	73.6	71.6	71.6	71.6	71.6	71.6	71.6
	Score	74	74	74	74	74	74	74	74	74	74	68	53	53	53	53	53	53	23	. 53
	Result. No.		~	٣	4	ស	9	7	æ	6	10	11	12	13	14	15	16	17	.18	19

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Sequence 7, Application US/10218509; Publication No. US20030092661A1; GENERAL INFORMATION: APPLICANT: Serrero, Ginette

US-10-218-509-7

RESULT 2

Sequence 2, Appli Sequence 307, App Sequence 11, Appl Sequence 11, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 28, Appl Sequence 28, Appl Sequence 397, Appl Sequence 377, Appl Sequence 1739, Appl Sequence 1739, Appl Sequence 1739, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 16, Appl Sequence 17, Appl	Sequence 24, Appl Sequence 160, App Sequence 4995, Ap Sequence 4973, Ap Sequence 5104, Ap Sequence 11, Appl
	10 US-09-918-909-24 110 US-09-789-561-160 9 US-09-764-891-4995 9 US-09-764-891-4973 9 US-09-764-891-5104 9 US-10-226-489-11
289 258 259 250 1156 275 275 275 275 275 275 275 275 275 275	1087 186 51 143 145
7717 7717 7717 7717 7717 7717 7717 771	0.04444 0.0844 0.0884 0.086
50 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	36.5 36.5 36 36 36
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	44444 112645

ALIGNMENTS

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Gaps
                                                                      APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
TITLE REPERENCE: 29996-488/P001-A
CURRENT PELING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,862
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)..(14)
OTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 74; DB 9; Length 14; 100.0%; Pred. No. 1.6e-06; Live 0; Mismatches 0; Indels
Sequence 7, Application US/09824647 Publication No. US20020183270A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ARRGTKCLRREAPR 14
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                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Human granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: PEPTIDE
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LOCATION: (1)..(14)
OTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
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100.0%; Pred. No. 1.6e-06;
Live 0; Mismatches 0;
                                    PRIOR APPLICATION NUMBER: 08/09/813,1,1 PRIOR APPLICATION NUMBER: 08/991,862 PRIOR FILING DATE: 1997-12-16; PRIOR PEPLICATION NUMBER: 08/863,862 PRIOR FILING DATE: 1997-05-23; NUMBER OF SEQ ID NOS: 17 SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 7
            FILE REFERENCE: 29996.488/P001-A
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Best Local Similarity 100.0
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
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Matches 14; Conservative
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ORGANISM: Human granulin
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US-09-824-647-17
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                                                                                                                                                                                                                                             LENGTH: 14
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                                                                                                                                                                                                                                                                     TYPE: PRT
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PUBLICANT: SETENCE 1.00108950A1

GENERAL INFORMATION:
APPLICANT: SETENCE 1.2996.488/P001-A

FILLE REFERENCE: 29996.488/P001-A

CURRENT APPLICATION NUMBER: US/08/991,862

PRIOR APPLICATION NUMBER: US/08/991,862

PRIOR APPLICATION NUMBER: 08/863,862

PRIOR APPLICATION NUMBER: 08/863,862

PRIOR FILING DATE: 1998-08-17

PRIOR FILING DATE: 1997-05-23

FRIOR FILING DATE: 1997-05-23

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 7
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TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS FILE REFERENCE: 29996.488/P001-A CURRENT APPLICATION NUMBER: US/10/218,509
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1998-08-17
PRIOR PLICATION NUMBER: 08/863,862
PRIOR FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)...(14)
OTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATION: (1)..(14)

OTHER INFORMATION: Internal peptide of human GP88 used to develop

OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
US-10-281-160-7
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TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 14;
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100.0%; Pred. No. 1.6e-06;
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; Patent No. US20020061859A1
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 14; Conservative
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Matches 14; Conservative
                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Human granulin
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Gaps

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Length 14; Indels

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Gaps
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OTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody.
                                                                                          APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 2996.488/P001-A
CURRENT APPLICATION WIMBER: US/09/824,807
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION UNDERE: 08/991,862
PRIOR PELICATION UNDERE: 08/981,862
PRIOR PELICATION NUMBER: 08/863,862
PRIOR FILING DATE: 1997-12-16
PRIOR FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 17, Application US/09824647; Publication No. US20020183270A1; GENERAL INFORMATION: APPLICANT: Serrero, Ginette; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS; FILE REFERENCE: Z9996.488/P001-A
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Sequence 7, Application US/09824807
Patent No. US20020094966Al
GENERAL INFORMATION:
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Gaps

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Indels

Length 593;

100.0%; Score 74; DB 9; 100.0%; Pred. No. 7.8e-05;

Mismatches

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1 ARRGIKCLRREAPR 14
                                                                           Best Local Similarity 100.
Matches 14; Conservative
 ; ORGANISM: Human GP88 cDNA US-10-281-160-17
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US-09-813-156-17
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                                                         Query Match
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APPLICANT: SETECTO, GINETTE
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001.A
CURRENT APPLICATION NUMBER: US/10/281,160
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: US/08/991,862
PRIOR PILING DATE: 1998-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: SETTETC, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/10/218,509
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR PILING DATE: 1998-08-17
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CURRENT APPLICATION NUMBER: US/09/824,647
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17
PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 17
LENGTH: 593
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Pred. No. 7.8e-05
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 08/863,862 PRIOR FILING DATE: 1997-05-23 NUMBER OF SEQ ID NOS: 17
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PRIOR FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/10281160
Publication No. US20030108950A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17, Application US/10218509 Publication No. US20030092661A1
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100.0%;
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Best Local Similarity 100.0%;
Matches 14; Conservative 0;
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566 ARRGTKCLRREAPR 579
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Best Local Similarity 100.0
Matches 14; Conservative
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SEQ ID NO 17
LENGTH: 593
TYPE: PRT
                                                                                                                                                                                       ; TYPE: PRT; ORGANISM: Human GP88 CDNA
US-09-824-647-17
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US-10-218-509-17
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LENGTH: 593
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Gaps
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TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996-188/P001-8
CURRENT APPLICATION NUMBER: US/09/824,807
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR APPLICATION NUMBER: 08/863,862
PRIOR FILING DATE: 1997-05-23
                                                             GENERAL INFORMATION:

APPLICANT: Serrero, Ginette
TITLE OF INFORMATION:
FILE REFERENCE: 29996.488 FOO1-8
CURRENT APPLICATION NUMBER: 08/09/813,156
CURRENT APPLICATION NUMBER: 08/991,862
PRIOR PELING DATE: 1997-12-16
PRIOR FILING DATE: 1997-12-16
PRIOR FILING DATE: 1997-05-23
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7.8e-05;
thes 0;
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Pred. No. 7.8e-05;
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Pred. No.
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Patent No. US20020094966A1
GENERAL INFORMATION:
                                 Sequence 17, Application US/09813156 Patent No. US20020061859A1
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 593
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SOFTWARE: Patentin Ver. 2:0
SEQ ID NO 17
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Best Local Similarity 100.0
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Best Local Similarity 100.
Matches 14; Conservative
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RESULT 9
US-09-813-156-17
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APPLICANT: Serrero, Ginette
TITLE DOFINITATION SERVENCE BROATUMORICENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 2099-648-7001-A
CURRENT APPLICATION NUMBER: US/10/218,509
CURRENT FILING DATE: 2002-08-15
PRIOR PILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 5:
LENGTH: 14
                                                                                                                                                                                                                                                                                                         ; LOCATION: (1)...(14)
; OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the ; OTHER INFORMATION: antisera against the GP88 used in the ; OTHER INFORMATION: Immunoaffinity step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-813-156-5 ; Sequence 5, Application US/09813156
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Best Local Similarity 75.0%;
Matches 9; Conservative 5
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75.0%;
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Best Local Similarity 75.0%
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Publication No. US20020183270A1

GENERAL INFORMATION:
JAPLICANT: Serrero, Ginette
JITLE OF INVENTION:
CURRENT PETRICE: 2996-488/P001-A

CURRENT FILING DATE: 2096-488/P001-A

CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,862

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,862

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/863,862

PRIOR PILING DATE: EARLIER FILING DATE: 1997-05-23

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 2.0
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OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the OTHER INFORMATION: antisera against the GP88 used in the OTHER INFORMATION: immunoaffinity step.
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                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: FALS
CURRENT PILITIG DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US/09/925,301
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 621;
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Pred. No. 0.00092;
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                                       Sequence 1416, Application US/09925301
Patent No. US20020052308A1
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Publication No. US20030092661A1
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75.0%;
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92.9%;
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Best Local Similarity 75.0°,
Post 9; Conservative
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Best Local Similarity 92.9
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
US-09-925-301-1416
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LENGTH: 621
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US-10-281-160-5

Sequence 5, Application US/10281160

Sequence 5, Application US/10281160

Publication No. US20030108950A1

GENERAL INFORMATION:
APPLICANT: Serrero, Ginette
FILE OF INVENTION: 88 RADA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996-488/P001-A

CURRENT APPLICATION NUMBER: US/10/281,160

CURRENT FILING DATE: 2002-10-28

PRIOR FILING DATE: 1998-08-17

PRIOR FILING DATE: 1998-08-17

PRIOR FILING DATE: 1998-08-17

PRIOR FILING DATE: 1997-05-23

NUMBER OF SEQ ID NOS: 120

SOFTWARE: Patentin Ver. 2.0
                                                               Gaps
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COTER INFORMATION: Internal peptide of mouse GP88 used to raise the OTHER INFORMATION: antisera against the GP88 used in the CTHER INFORMATION: immunoaffinity step.
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Score 53; DB 9; Length 14;
Pred. No. 0.0072;
2; Mismatches 1; Indels
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Pred. No. 0.0072;
2; Mismatches 1; Indels
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICATION:
APPLICATION:
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
CURRENT PELING DATE: 2001-03-21
PRIOR PILING DATE: 1997-12-16
FRIOR PILING DATE: 1997-12-16
FRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 14
TYPE: PRT
ORGANISM: mouse granulin
FEATURE:
RATORE:
NAME/REY: PEPTIDE
LOCATION: (1)..(14)
OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the
OTHER INFORMATION: immunoaffinity step.
US-09-813-156-5
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Gaps

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Query Match
71.6%; Score 53; DB 10; Length 14;
Best Local Similarity 75.0%; Pred. No. 0.0072;
Matches 9; Conservative 2; Mismatches 1; Indels

Search completed: July 8, 2003, 16:31:42 Job time: 13.641 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

8, 2003, 16:19:45 ; Search time 14.1795 Seconds (without alignments) 94.918 Million cell updates/sec July Run on:

US-09-824-647-7 74 Title: Perfect score: Sequence:

1 ARRGIKCLRREAPR 14

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

283224 Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

PIR_73:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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•	,	Description	granulin precursor	epithelin/granulin	epithelin/granulin	nicotinate-nucleot	hypothetical prote	gastric mucin rela	sucrose-phosphate	RNA2 polyprotein -	hypothetical prote	hypothetical prote	exopolyphosphatase	MCM / cell divisio	hypothetical prote	hypothetical prote	acetyl-CoA carboxy	sucrose-phosphate	allergen - rice	hypothetical prote	hypothetical prote	adenine deaminase-	mannosyl transfera	methyl-accepting c	hypothetical prote	sucrose-phosphate	sucrose-phosphate	hypothetical prote	sucrose-phosphate	Q,	hypothetical prote
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		a :	GYHU	C38	B38	A7557	T4951	T4951	T04	S06187	T19	G70	T20	H84	T08	070	C75	301	T02	AG2	T24	C75	AF2	A87	T22	151	Š	F86	T09	T04	E72
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A;Molecule type: protein A;Residues: 364-367, X',369-385,'H',387-396 <BA3> A;Note: this protein was purified and characterized as granulin C A;Accession: D36698

A; Residues: 442-446, 'XDTSS', 456-458, 'DG' <BA4>

A; Molecule type: protein

granulin

A; Molecule type: protein A; Residues: 206-218, 'H', 220-233 <BA2> A; Note: this protein was purified and characterized as A; Accession: C36698

A;Molecule type: protein A;Residues: 281-336 <BAT> A;Note: this protein was purified and characterized as granulin A;Accession: B36698

	nypornerical prote hypothetical prote	porphobilinogen de	protein R09E10.1 [hypothetical prote	HYA22 protein - hu	r40gg protein - ri	sucrose-phosphate	DNA-binding protei	related to suppres	DNA-directed RNA p	probable vitelloge	ALR protein - huma	ALR protein - huma	bcl-2-associated p	
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AH3346	T24091 F71294	G87257	H88808	T15837	JC5707	T03960	872650	S61413	T49868	\$35548	T13171	T03455	T03454	C47538	
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30	31	3.6	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT 1 GYHU granulin precursor [validated] - human
N;Alternate names: epithelin N;Contains: granulin A; granulin B; granulin C; granulin D; granulin E; granulin
C; Species: Homo saptens (man) C; Date: 30-Sep-1992 #sequence_revision 03-May-1996 #text_change 08-Dec-2000 C: Accession: J71284: A38118; A3818; B36698; B36698; C36698; D36698; A56873
R; Bhandari, V.; Bateman, A.
Blochem. Blophys. Mes. Commun. 186, 27-03, 1934. A; Title: Structure and chromosomal location of the human granulin gene.
A; Reference number: JC1284; MUID:93038/04; PMID:141/868 A:Accession: JC1284
A Molecule type: DNA
A; restuces; 1.93 carry, Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Tod: R; Plowman, G.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Tod: R; Plowman, G.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Tod: R; Plowman, G.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Tod: R; Plowman, G.D.; McDonald, G.D.; McDonald, V.L.; Tod: R; Plowman, G.D.; McDonald, V.L.; Tod: R; Plowman, G.D.; McDonald, G.
J. Biol. Chem. 267, 13073-13078, 1992
A;Title: The epithelin precursor encodes two proteins with opposing activities of
A; Reference number: Assizo; MoiD: 3431/004; FMID: 101003 A; Accession: A38128
A; Status: preliminary
A; Molecule type: mRNA A: Regidues: 1-593 <plo></plo>
A; Cross-references: GB:X62320; NID:g31192; PIDN:CAA44196.1; PID:g31193
R;Bhandari, V.; Palfree, R.G.E.; Bateman, A.
Proc. Natl. Acad. Sci. U.S.A. 89, 1715-1719, 1992
A.Title: Isolation and Sequence of the grantin precursor cura from number a pacter of a page 154265
A; Accession: A38118
A; Molecule type: mRNA
A; Residues: 1-406, 'R', 408-433, 'G', 435-453, 'G', 455-459, 'Q', 461-546, 'R', 548-566, 'R
A;Cross-references: GB:M/Jib; NID:GHB3b12; PID:AAA3001/.1; FID:G103013
Ayouce: Lils sequence may been revised in restaurce of the payable
Biochem Blophys Res. Commun. 173, 1161-1168, 1990
A; Title: Granulins, a novel class of peptide from leukocytes.
A; Reference number: A36698; MUID: 91097544; PMID: 2268320
A Accession: A 3 6 6 9 8
A:Molecule type: protein

Gaps

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C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Sate: 10-Jul-1992, #sequence_revision 10-Jul-1992 #text_change 20-Aug-1999
C; Accession: B38128; A36199; B36698; T53272
R; Plowman, G.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Todarc
J. Biol. Chem. 267, 13073-13078, 1992
A; Title: The epithelin precursor encodes two proteins with opposing activities on e
A; Reference number: A38128; MUID: 92317004; PMID: 1618805
A; Recession: B38128
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;Residues: 1-589 <-PLO>

;Cross-references: GB:X62322; NID:956108; PIDN:CAA44198.1; PID:956109

;Cross-references: GB:X62322; NID:956108; PIDN:CAA44198.1; PID:956109

;Shoyab, M.; McDonald, V.L.; Byles, C.; Todaro, G.J.; Plowman, G.D.

roc. Natl. Acad. Sci. U.S.A. 87, 7912-7916, 1990

;Title: Epithelins 1 and 2: isolation and characterization of two cysteine-rich gr
;Recession: A36199; MUID:91045907; PMID:2236009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :Title: The complementary deoxyribonucleic acid sequence, tissue distribution, and :Reference number: 153272; MOID:94062640; PMID:8243292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase - Deinococcus
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 %sequence_revision 03-Dec-1999 %text_change 02-Mar-2001
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R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R
                                                                                                                 A;Wolecule type: protein
A;Residues: 18-19,'X',21-25,'X',27-29,'XX',32;'XXX',119-127;152-154,'DXK',158-161,'
C;Superfamily: granulin
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A;Cross-references: GB:M97750; NID:g204223; PIDN:AAA16903.1; PID:g204224
                                                                                                                                                                                                                                                                                                     Length 589;
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Residues: 205-226 <SHRD.
Bateman, A.; Belcourt, D.; Bennett, H.; Lazure, C.; Solomon,
lochem. Biophys. Res. Commun. 173, 1161-1168, 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'SB',310-324,'T',326,'X',328,'Q' <BAT>
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0.12;
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Pred. No. 0.29;
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Pred. No.
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66.7%;
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Best Local Similarity 75.0%;
Matches 9; Conservative
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564 KGTKCLRKKTPR 575
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sidues: 280-300 <SHO>
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nes 8; Conserv
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                                                                           A;Status: preliminary
                            A; Accession: A46705
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R; Kardana, A.; Bagshawe, K.D.; Coles, B.; Read, D.; Taylor, M.

Br. J. Cancer 67, 686-692, 1993

A; Title: Characterisation of UGP and its relationship with beta-core fragment.

A; Reference number: A56873; MUID:93229246; PMID:8471426

A; Accession: A56873; MUID:93229246; PMID:8471426

A; Molecule type: protein

A; Molecule type: protein

A; Residues: 281-283, 'x', 285-289, 'S', 291-295 < KAR>

A; Rosidues: 281-283, 'x', 285-289, 'S', 291-295 < KAR>

A; Rote: sequence extracted from NCBI backbone (NCBIP:129524)

C; Genetics:

A; Note: sequence extracted from NCBI backbone (NCBIP:129524)

A; Gene: GDB:GRN

A; Cross-references: GDB:136006; OMIM:138945

A; Map position: 17pter-17qter

A; Introns: 46/3; 88/3; 117/1; 154/3; 200/1; 236/3; 279/1; 311/3; 393/3; 471/3; 548/3

C; Superfamily: granulin

C; Keywords: glycoprotein: tandem repeat

F; 117/Domain: signal sequence extratus predicted <AMIP>
F; 18-593/Product: granulin #status predicted <AMIP>
F; 18-593/Product: progranulin #status predicted <PRO>
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A.Residues: 18-349, L', 351-589 <BAB>
A.Residues: 18-349, L', 351-589 <BAB>
R.Baba, T.; Hoff, H.B.
MOL. Reprod. Dev. 34, 233-243, 1993
A.Title: Acrogranin, an acrosomal cysteine-rich glycoprotein, is the precusor of the grd
A.Reference number: 149468
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Residues: 1-250, L', 252-253, V', 255-349, L', 351-401, SA', 404-589 <RES>
A.Residues: 1-250, L', 252-253, V', 255-349, L', 351-401, SA', 404-589 <RES>
A.Cross-references: GB:M86736; NID:9191766; PIDN:AAA37191.1; PID:9191767
B.Zhou, J.; Gao, G.; Crabb, J.W.; Serrero, G.
J. Biol. Chem. 268, 10863-10869, 1993
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W.Alternate names: acrogranin; Pc-cell-derived growth factor
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 20-Aug-1999
C.Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 20-Aug-1999
C.Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 20-Aug-1999
S.Plowman, G.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Todaro, G.J.
J. Biol. Chem. 267, 13073-13078, 1992
J. A.Title: The epitchalin precursor encodes two proteins with opposing activities on epithe A; Reference number: A38128; MUID:92317004; PMID:1618805
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A:Reference number: S32503; MUID:93245991; PMID:8482392
A:Accession: S32503
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A;Title: Purification of an autocrine growth factor homologous with mouse epithelin pred
A;Reference number: A46705; MUID:93266526; PMID:8496151
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A; Residues: 1-589 <PLO>
A; Cross-references: GB:X62321; NID:950851; PIDN:CAA44197.1; PID:950852
R; Baba, T.; Nemoto, H.; Watanabe, K.; Arai, Y.; Gerton, G.L.
FEBS Lett. 322, 89-94, 1993
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Pred. No. 0.00025;
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llarity 92.9%;
Conservative
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Matches 13; Conserv
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Length 422;

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C;Accession: T04062
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Maye.
Bubuitted to the Protein Sequence Database, March 1999
A;Reference number: Z15184
A;Accession: T04062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: S06187
R; Brault, V.; Hibrand, L.; Candresse, T.; le Gall; O.; Dunez, J.
Mucleic Acids Res. 17, 7809-7819, 1989
A; Ittle: Nucleotide sequence and genetic organization of Hungarian grapevine chr. A; Reference number: S06187; MUID: 90016865; PMID: 2798129
A; Accession: S06187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase hor F;230-714/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 4
A;Introns: 86/3; 116/3; 255/3; 322/2; 482/3; 526/3; 570/3; 629/3; 647/3; 668/3;
A;Note: F28M11.40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A. Residues: 1-1324 <BRA>
A:Cross-references: EMBL:X15163; NID:959347; PIDN:CAA33255.1; PID:959348
A:Note: part of this sequence, including the amino end of the coat protein, was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA2 polyprotein - grapevine chrome mosaic virus
N:Contains: coat protein
C;Species: grapevine chrome mosaic virus
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                 sucrose-phosphate synthase homolog F28M11.40 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Experimental source: cultivar Columbia; BAC clone F28M11
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Pred. No. 31;
0; Mismatches
                           DB 2;
13;
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Pred. No. 37;
1; Mismatches
                                                                                2; Mismatches
                           Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-1083 <BEV>
A; Cross-references: EMBL: AL049487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.4%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 55.4%;
Local Similarity 61.5%;
Les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 468 RRGVSCLGRYMPR 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 RRGTKCLRREAPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 RHGTRCLRHGGP 138
                                                                                                                                                                   :|| :||| | |
370 QRGPQCLRRRPP 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 55.4
Best Local Similarity 58.3
Matches 7; Conservative
                                                       Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 RRGTKCLRREAP 13
                                                                                                                                  2 RRGTKCLRREAP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position; segment S2
A; Introns: 960/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Keywords: polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 8
                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
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, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Md
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: T49513
;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
ubmitted to the Protein Sequence Database, May 2000
                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: Pseudomonas nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltrd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
A;Reference number: 225022
                                                                                                                                                                                                                                            A;Cross-references: GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF12397.1; PID:g646069
                                                                                A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gastric mucin related protein [imported] - Neurospora crassa
N;Alternate names: protein B1406.650
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Neurospora crassa
Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
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A;Experimental source: BAC clone B14D6; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.660
A;Experimental source: BAC clone B14D6; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43; DB 2; Length 365;
Pred. No. 5.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pothetical protein B14D6.660 [imported] - Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 11;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                58.1%;
ilarity 81.8%;
Conservative
                                                                                                                                                                                                                                                                     A; Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|| :||| |
275 QRGPQCLRRRPP 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1111: |||||
146 RRGTRNLRREA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 58.3
hes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RRGTKCLRREAP 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: 225022
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-365 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-327 <SCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: NCSP:B14D6.650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Gene: NCSP:B14D6.660
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Molecule type: DNA
                                                                                                                                                                 A; Status: preliminary
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A; Introns: 93/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 6
                                                                                                                                                                                                                                                                                                                                                     A; Map position: 2
                                                                                                                                                                                                                                                                                                                          A; Gene: DRA0240
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Matches
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Length 1324;

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R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; La: Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.I.A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE004437; NID:g10581599; PIDN:AAG20316.1; GSPDB:GN00138
C;Genetics:
A;Gene: mcm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C;Accession: T08723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCM / cell division control protein 21 [imported] - Halobacterium sp. NRC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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hypothetical protein Rv1312 - Mycobacterium tuberculosis (strain H37RV)
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submitted to the Protein Sequence Database, March 1999
A;Reference number: 216473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AL050051
A;Experimental source: fetal kidney; clone DKF2p566D193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein DKFZp566D193.1 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 2;
Pred. No. 9.9;
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                                                                                                                                                                                Score 40; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             core 40; DB;
red. No. 37;
Mismatches
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                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40;
Pred. No.
                                                                                                                                                                                                                        Pred. No
   A; Experimental source: strain IL144 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.7%;
77.8%;
                                                                         A;Gene: ppx
C;Superfamily: exopolyphosphatase
                                                                                                                                                                                54.18;
61.58;
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66.7%;
                                                                                                                                                  Query Match
Best Local Similarity 61.5.
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                338 RRATKVWKREAP 349
                                                                                                                                                                                                                                                                                                                        2 RRGTKCLRREAPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 66.7
Matches 8; Conservative
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Best Local Similarity
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A; Residues: 1-118 < KOE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-831 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Appothetical protein Rv2084 - Mycobacterium tuberculosis (strain H37RV)

(Species: Mycobacterium tuberculosis

(Species: Mycobacterium tuberculosis from the complete genome A; Rollaton, J.E.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Saquares, S.; Segers, J.; Rutter, S.; Segert, K.; Skelton, S.; Squares, S.

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C;Species: Rubrivivax gelatinosus
C;Species: Rubrivivax gelatinosus
C;Species: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 18-Aug-2000
C;Accession: T50868
R;Nagashima, K.V.; Igarashi, N.; Harada, J.; Nagashima, S.; Matsuura, K.; Shimada, K.
submitted to the EMBL Data Library, November 1999
A;Description: Determination of Nucleotide Sequences of Rubrivivax gelatinosus Photosynt
A;Reference number: 225270
A;Accession: T50868
A;Coss-references: EMBL;AB034704; PIDN:BAA94021.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:Z73966; GB:AL123456; NID:g3261577; PIDN:CAA98196.1; PID:g1370250 A;Experimental source: strain H37Rv C; Genetics: C; Genetics: A;Gene: Rv2084 C;Superfamily: Mycobacterlum tuberculosis hypothetical protein Rv2084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL: Z80215; PIDN: CAB02276.1; GSPDB: GN00019; CESP: C36B1.11
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19782
R;Lennard, N.
R;Lennard, N.
R;Lennard, N.
R;Reference number: 21976
A;Reference number: 21976
A;Reference number: 21976
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-327 <WILL>
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Pred. No. 18;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 1
A;Introns: 83/3; 125/3; 174/3; 197/1; 261/3; 323/2
                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: clone C36B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.18;
71.48;
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SRRFEMCIRRESP 286
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Best Local Similarity 71.4
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 53.8
Matches 7; Conservative
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Length 831

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Length 118;

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R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; , M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .Cross-references: GB:AE001874; GB:AE000513; NID:96457778; PIDN:AAF09708.1; PID:9645778
Experimental source: strain R1
                                                                             R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Asjandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acetyl-CoA carboxylase, bitoin carboxyl carrier protein - Deinococcus radiodurans (strai
C;Species: Deinococcus radiodurans
                                                                                                                                               A; Filte: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:273419; GB:AL123456; NID:93261573; PIDN:CAA97745.1; PID:91322436
A;Experimental source: strain H37Rv
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. Reference number: A75250; MUID:20036896; PMID:10567266
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C;Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology
                                                                                                                                                                                                                                                                                           A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
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Pred. No. 12;
3; Mismatches 4; Indels
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Pred. No. 22;
2; Mismatches
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50.0%;
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Best Local Similarity 53.8%;
Matches 7; Conservative
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78 SRRGVEIISRRAPR 91
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Best Local Similarity
Matches 7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: DNA
Residues: 1-187 <WHI>
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 8, 2003, 16:16:30; Search time 6.82051 Seconds (without alignments) 85.136 Million cell updates/sec Run on:

US-09-824-647-7 74 1 ARRGTKCLRREAPR 14 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched: 112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

287 1 YKFA ECOLI 337 1 VINT BPP2 444 1 GDF9 JMOUSE 673 1 Y552_HUMAN 821 1 CTRI_ARATH 843 1 BLVR_BOVIN 916 1 CHSB_EMENI
97.5 821 843 843 916 2411 67

026960 methanobact	Q12170 pseudomonas	P40578 saccharomyc	P03833 klebsiella P03189 epstein-bar	Q050th oryctolagus	Q05318 ebola virus	054898 rattus norv	043497 homo sapien	P17053 paramecium	
HEM3_METTH	PPX_PSEAE	NEK4_HUMAN MGA2_YEAST	NIFJ_KLEPN V120 EBV	PHLX_RABIT	RRPL_EBOZM	CCAG_RAT	CCAG_HUMAN	G168_PARPR	
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45.9	6.54	45.9 6.03	45.9	45.9	45.9	45.9	45.9	45.9	١
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34	36	38	39	41	42	43	44	45	

ALIGNMENTS

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RESULT 1

RT "Granulins, a novel class of peptide from leukocytes.";
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us-09-824-647-7.rsp

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Best Local Similarity
Matches 9; Conserv
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CARBOHYD
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        SOURCE THE TEST TEST TO DESCRIPTION OF THE PROPERTY OF THE PRO
                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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FUNCTION: GRANULINS HAVE POSSIBLE CYTOKINE-LIKE ACTIVITY. THEY MAY PELAY A ROLE IN INFLAMMATION, WOUND REPAIR, AND TISSUE REMODELING. FUNCTION: GRANULIN A PROMOTES PROLIFERATION OF THE EPITHELIAL CELL LINE A431 IN CULTURE WHILE GRANULIN B ACTS AS AN ANTAGONIST TO GRANULIN A, INHIBITING THE GROWTH. I (shown here) and 2; may be produced by alternative splicing.

TISSUE SPECIFICITY: IN WIELOGENOUS LEUKEMIC CELL LINES OF PROMONOCITIC, PROMIECCTIC, AND PROBRYTHROID LINEMGE, IN FIBROBLASTS, AND VERY STRONGLY IN PPITHELIAL CELL LINES. PRESENT IN INFLAMMATORY CELLS AND BONE MARROW. HIGHEST LEVELS IN KIDNEY. PTM: GRANULINS ARE DISULFIDE BRIDGED.
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Cytokine; Repeat; Glycoprotein; Signal; Alternative splicing;
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N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
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Pred. No. 9.8e-05;
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GRANULIN 5.
GRANULIN 6.
GRANULIN 7.
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GRANULIN 3.
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EMBL; X62320; CAA44196.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000118; Granulin.
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92.98;
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SMART; SM00277; GRAN; 7.
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386
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2496
2573
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PIR; D36698; D36698.
PIR; JC1284; JC1284.
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593 AA;
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Best Local Similarity
Matches 13; Conserv
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SIGNAL
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VARSPLIC
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PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                              Gaps
01-ocr-1994 (Rel. 30, Last sequence update)
16-ocr-2001 (Rel. 40, Last annotation update)
Granulins precursor (Acrogranin) [Contains: Granulin 1; Granulin 2;
Granulin 3; Granulin 4; Granulin 5; Granulin 6; Granulin 7].
                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .) (POTENTIAL)
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                                                                                                                                                                                                                                                               Baba T., Nemoto H., Watanabe K., Arai Y., Gerton G.L.; "Exon/introf organization of the gene encoding the mouse epithelin/granulin precursor (acrogranin)."; FEBS Lett. 322:89-94(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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ACROGRADIN.
GRANULIN 1.
GRANULIN 2.
GRANULIN 3.
GRANULIN 4.
GRANULIN 6.
GRANULIN 6.
GRANULIN 7.
N-LINKED (GLCNAC...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 53; DB 1;
Pred. No. 0.049;
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                                                                                                                                                                                                                                             MEDLINE-93245991; PubMed-8482392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00799; GRANULINS; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000118; Granulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63458 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D16195; BAA03736.1; -.
EMBL; M86736; AAA37191.1; -.
EMBL; X62321; CAA44197.1; -.
MGD; MGI:95832; Grn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.6%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            564 RGTKCLRKKIPR 575
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2493
2568
                                                                                                              musculus (Mouse)
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589 AA.

PRT;

GRN MOUSE STANDARD; B P28798; 01-DEC-1992 (Rel. 24, Created)

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RESULT 2

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RESULT

us-09-824-647-7.rsp

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HSSP; Q05603; 1
TIGR; DRA0240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plowman G.D., Green J.M., Neubauer M.G., Buckley S.D., McDonald V.L., Todaro G.J., Shoyab M.;

"The epithelin precursor encodes two proteins with opposing activities on epithelial cell growth.";
J. Biol. Chem. 267:13073-13078(1992).
                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                             01-NOV-1991 (Rel. 20, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-CGT-2001 (Rel. 40, Last annotation update)
Granulins precursor (Acrogranin) {Contains: Granulin 1 (Granulin G);
Granulin F); Granulin F); Granulin B) (Epithelin 2);
Granulin 4 (Granulin A) (Epithelin 1); Granulin E);
Granulin 6 (Granulin D); Granulin 7 (Granulin E)].
                                                                                                                                                                                                                                                                                                                                                                                                                 G.D.;
                                                                                                                                                                                                                 Bhandari V., Giaid A., Bateman A.; "The complementary deoxyribonucleic acid sequence, tissue distribution, and cellular localization of the rat granulin
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-91045907; PubMed-2236009; Shoyab M., McDonald V.L., Byles C., Todaro G.J., Plowman G. Epithellins 1 and 2: isolation and characterization of two cysteine-rich growth modulating proteins."; Proc. Natl. Acad. Sci. U.S.A. 87:7912-7916(1990).
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE OF 204-259 AND 278-334.
         Ä.
         588
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ACROGRANIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00799; GRANULINS; 7.
Cytokine; Repeat; Glycoprotein; Signal.
         PRT;
                                                                                                                                                                                                                                                               3ndocrinology 133:2682-2689(1993)
                                                                                                                                                                                                                                                                                                           MEDLINE-92317004; PubMed-1618805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-91097544; PubMed-2268320;
                                                                                                                                                                                                     MEDLINE-94062640; PubMed-8243292;
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 204-225 AND 279-299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000118; Granulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M97750; AAA16903.1; -. EMBL; X62322; CAA44198.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00396; granulin; 7.
SMART; SM00277; GRAN; 7.
         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE OF 278-328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A36199; A36199.
PIR; B36199; B36199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; E36698; E36698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISSUE-Bone marrow;
                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                           NCBI_TaxID-10116;
                                                                                                                                                                                                                                                     recursor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last amotation update)
Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase
(EC 2.4.2.21) (NN:DBI PRT) (N(1)-alpha-phosphoribosyltransferase).
COBT OR DRA0240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: CATALYZES THE SYNTHESIS OF ALPHA-RIBAZOLE-5'-PHOSPHATE FROM NICOTINATE MONONUCLEOTIDE (NAMN) AND 5,6-
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WEDLINE-20036896; PubMed=10567266; White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Wamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dimethylbenzimidazole = nicotinate + N(1)-(5-phospho-alpha-D-
ribosyl)-5,6-dimethylbenzimidazole.
                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
                                                                                                                                                                                                                                                                                                                                                             Score 51; DB 1; Length 588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: Beta-nicotinate D-ribonucleotide
                                                                                                                                                                                                                                                                                                              113D434F7E099B31 CRC64;
                                                                                                                                                                                                                                                                O -> T (IN REF. 4).
M -> I (IN REF. 2).
                                                                                                                                                                                       N-LINKED (GLCNAC. S -> FP (IN REF. 2)
TK -> SB (IN REF. 4
                                                                                                                                          (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATHWAY: Cobalamin biosynthesis.
SIMILARITY: BELONGS TO THE COBT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
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                                                                   GRANULIN GRANULIN GRANULIN GRANULIN N-LINKED N-LINKED N-LINKED
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16-OCT-2001 (Rel. 40, Last seq
                                                                                                                                                                                                                                                                                                                63369 MW;
                                                                                                                                                                                                                                                                                                                                                                68.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 286:1571-1577(1999)
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                                                                                                                                                                                                                                                                                                                                                                                         66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      563 KGTKCLRKKTPR 574
                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 RGTKCLRREAPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deinococcus radiodurans.
                                                                                                                                                                                                                                                                                                              588 AA;
                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                          438
512
38
372
525
525
307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COBT_DEIRA Q9RYR8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-R1;
                                                                                                                                                                                                                                          CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                               CARBOHYD
                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                            CARBOHYD
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Q05603; 1D0V.

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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF THE VIRUS.

PTH: THE TRAZ POLYPROTEIN IS CLEAVED BY AN RNAL-ENCODED PROTEASE
TO YIELD THE MATURE COAT PROTEIN AND AN 84 KDA PROTEIN WHICH IS
FURTHER CLEAVED INTO TWO PRODUCTS OF APPROXIMATELY 46 AND 48 KDA.
SIMILARITY: TO THE RNAZ POLYPROTEIN OF OTHER NEPOVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chrome mosaic nepovirus RNA2.";
Nucleic Acids Res. 17:7809-7823(1989).
-1- FUNCTION: THE PROTEIN LOCATED AT THE N-TERMINAL END OF THE
NEPOVIRUS POLYPROTEIN COULD BE REQUIRED FOR NEMATODE TRANSMISSION
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 814-822.
MEDIATE-90016865; PubMed-2798129;
Brault V., Hibrand L., Candresse T., le Gall O., Dunez J.;
"Nucleotide sequence and genetic organization of Hungarian grapevine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                             01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
RNA2 polyprotein (147 kDa protein) [Contains: Coat protein; 84 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                      Hungarian grapevine chrome mosaic virus (GCMV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;
                                                                                                                                                          ö
          Pfam; PF02277; DBL_PRT; 1.
Cobalanin blosynthesis; Porphyrin blosynthesis; Transferase;
Complete proteome.
ACT_SITE 330 BASE (BY SYMILARITY).
SEQUENCE 365 AA; 37265 MW; 81A37D3194F2EC7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 1; Length 1324;
Pred. No. 16;
1; Mismatches 4; Indels
                                                                                                                     58.1%; Score 43; DB 1; Length 365; 81.8%; Pred. No. 1.9;
                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302C286B2EA1756A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 KDA PROTEIN
                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COAT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N -> D.
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InterPro; IPR005305; Nepo_coat_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR005306; Nepo_coat_N. Pfam; PF03391; Nepo_coat; 1. Pfam; PF03689; Nepo_coat_C; 1. Pfam; PF03689; Nepo_coat_M; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147804 MW;
InterPro; IPR003200; NN:DBI_PRT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X15163; CAA33255.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coat protein
                                                                                                                                      Local Similarity 81.8 es 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                       2 RRGTKCLRREA 12
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1324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=12273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polyprotein;
                                                                                                                                                                                                                                                                                                             POL2_GCMV
P13026:
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                        protein]
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POL2_GCMV
ID POL2 (
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2 RRGIKCLRREAP 13

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harris D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Elglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devins K., Feltwell T., Gentles S., Hamin N., Holroyd & Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l protein; Complete proteome.
380 AA; 41314 MW; D61A51A1BC8775EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 1;
Pred. No. 6.8;
0; Mismatches
                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
19-pothetical protein Rv2084.
RV2084 OR MT2146 OR MTCX49.23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z73966; CAA98196.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98295987; PubMed-9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YD12_MYCTU STANDARD; E Q10620; 01-0CT-1996 (Rel. 34, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis.
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127 RHGTRCLRHGGP 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ruberculist; Rv2084; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical
SEQUENCE 34
                                                                                                                                                                                    YK84_MYCTU
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ID YD12_M)
AC Q10620;
DT 01-OCT-
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. By any and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ilensia.ch).
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                                                                                                                                              adenovirus CELO.";
J. Virol. 70:2939-2949(1996).
-i- CATALXTIC ACTIVITY: N deoxynucleoside triphosphate - N'diphosphate
                                                                                                                                                                                                                                     -i- MISCELLANEOUS: THIS DNA POLYMERASE REQUIRES A PROTEIN AS A PRIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chondler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T., Siguler P., Thebault P., Whalen M., Wincker P., Levy M., Meissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002).
                                                                                                                 "The complete DNA sequence and genomic organization of the avian
                                                              Chiocca S., Kurzbauer R., Schaffner G., Baker A., Mautner V., Cotten M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 1; Length 1121;
Pred. No. 30;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00116; DNA_POLYMERASE_B; 1.
Transferase; DNA-directed DNA polymerase; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1121 AA; 129395 MW; A55B9B6A54D3BDE1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I - SIMILARITY: BELONGS TO THE UPF0125 (RNFH) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ralstonia solanacearum (Pseudomonas solanacearum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21681879; PubMed-11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U46933; AAC54904.1; -.
InterPro; IPR002064; DNA_pol_B.
InterPro; IPR004868; DNA_pol_B_2.
Pfam; PF03175; DNA_pol_B_2; 1.
PRINTS; PR00106; DNAPOLB.
                                           MEDLINE=96186720; PubMed=8627769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein RSc1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.7%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00486; POLBC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSC1426 OR RS05266
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[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=305;
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                                                                                                                                                                                                                         (DNA) (N)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08XZG9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YE26_RALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                 Gordon S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeler K., Gas S., Barry C.E. III, Tekaja F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Deviln K., Feltwell T., Gentles S., Hamiln N., Holroyd S., Honsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Ollver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DoBoy R., Cardon M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                      Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Avian adenovirus gall (strain Phelps) (Fowl adenovirus 1) (CELO). Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Aviadenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.7%; Score 39; DB 1; Length 147; 50.0%; Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aboratory strains.";
ubmitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ypothetical protein; Transmembrane; Complete proteome.
FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 AA; 16594 MW; A880FB972E48AE27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1- SIMILARITY: STRONG, TO M. LEPRAE ML1147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                       MEDLINE-98295987; PubMed-9634230;
                                              Hypothetical protein Rv1312.
Rv1312 OR MT1352 OR MTCX373.32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AE007008; AAK45614.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA polymerase (EC 2.7.7.7).
                                                                                                  Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ARRGTKCLRREAPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SREGVEIISREAPR 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z73419; CAA97745.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 50.0 nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "uberculist; Rv1312; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-10553;
                                                                                                                                                                          NCBI_TaxID-1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MT1352;
                                                                                                                                                                                                                                                     STRAIN-H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPOL_ADEG1
Q64751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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RESULT 8 DPOL ADEG1

Matches

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EMBL; TIGR;

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Gaps

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entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CSTEL, 63; TISSUB-Embryo;

X REDLINE-2108566) PubMed-11217851;
A RAWAI J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Rondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Rubil P., Lewis S., Matsuo Y., Mikaido I., Pesole G., Quackenbush J.,
Sakai K., Okido T., Futuno M., Anno H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
B. Hayashi, P. V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Mitochondrial precursor proteins import receptor (Translocase of outer
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- FUNCTION: RECEPTOR THAT ACCELERATES THE IMPORT OF ALL MITOCHONDRIAL PRECURSOR PROTEINS (BY SIMILARITY).
-1- SUBUNIT: FORMS PART OF THE RECEPTOR COMPLEX THAT CONSISTS OF AT LEAST 8 DIFFERENT PROTEINS (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                    ó
                                                                                                                                                                                          Score 38; DB 1; Length 118;
Pred. No. 4.8;
                                                                                                                                                                                                                                    4; Indels
                                                           EMBL; AL646064; CAD15128.1; -.
InterPro; IPR005346; UPF0125.
Pfam: PF03658; UPF0125; 1.
Hypothetial protein; Complete proteome.
SEQUENCE 118 AA; 12743 MW; C0594E56E184E769 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                611 AA.
                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              outer membrane (By similarity).
-1- SIMILARITY: CONTAINS 10 TPR REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                            51.4%;
                                                                                                                                                                      Ouery Match
Best Local Similarity 66./.
                                                                                                                                                                                                                                                                                                                      100 REGLKWLRNEAP 111
                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                           2 RRGTKCLRREAP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POMM70A OR D16WSU109E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            membrane TOM70)
                                                                                                                                                                                                                                                                                                                                                                                                                              OM70_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                            OM70_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
  SSSEE##
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagase T., Miyajima N., Tanaka A., Sazuka T., Seki N., Sato S., Tabbta S., Ishikawa K.-I., Kawarabayasi Y., Kotani H., Nomura N.; "Prediction of the coding sequences of unidentified human genes. III The coding sequences of 40 new genes (KIAA0081-KIAA0120) deduced by analysis of cDNA clones from human cell line KG-I.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                         Transmembrane; Repeat; TPR repeat.
                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                         Score 38; DB 1; Length 611;
Pred. No. 25;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                     INTERMEMBRANE (POTENTIAL).
                                                                                                                                                                                                                                                                               486FB79FC4CE5B4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 648 AA; 70463 MW; 88F68A62D6C1CDA1 CRC64;
                                                                                                                 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein KIAA0084 (HA2022) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.4%; Score 38; DB 58.3%; Pred. No. 27; Ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Bone marrow;
MEDLINE-95308325; PubMed-7788527;
                                                                                                                                                            TPR
TPR
TPR
TPR
HSSP; P53041; 1A17.
MGD; MG1:106295; D16Msu109e.
InterPro; IPR001440; TPR.
Pfam; PF00515; TPR; 10.
Micchondrion; Outer membrane; Tr
DOMAIN 1
                                                                                                                                                                                                                                                                                  67521 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D42043; BAA07644.1; -.
                                                                                                                                                                                                                                                                                                                                                                                        :||| |:::: |
375 KRGTMCMQQQQP 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 58.5.
7; Conservative
                                                                                                                                                                                                                                                                                                                                      5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                      2 RRGTKCLRREAP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ARRGTKCLRREA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Res. 2:37-43(1995).
                                                                                                                                                                           365
403
437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein
                                                                                                                                                                                                                                                                                  611 AA;
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                          404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y084_HUMAN
Q14699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KIAA0084.
                                                                                                      FRANSMEM
                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                     DOMAIN
                                                                                                                                               REPEAT
                                                                                                                                   REPEAT
                                                                                                                                                               REPEAT
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                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
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EMBL; AK012084; BAB28018.1; -.

41, Last sequence update)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SUBUNIT: HOMODIMER OR HOMOTETRAMER.
-i- DEVELOPMENTAL STAGE: GERMINATING SEEDS OR MATURE LEAVES.
-i- PIM: PHOSPHORYLATED. HOWEVER, PHOSPHORYLATION IS NOT ESSENTIAL FOR
                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade,
Panicoldeae, Andropogoneae, Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 71-74; 206-212; 471-481 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                         01-JUL-1993 (Rel. 26, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Sucrose-phosphate synthase (EC 2.4.1.14) (UDP-glucose-fructose-
phosphate glucosyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 1068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-GLY.
W; 074679B5E9AlD282 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF00534; Glycos_transf_1; 1.
Transferase; Glycosyltransferase; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     533 AA.
                                                                     1068 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001296; Glycos_transf_1.
                                                                                                                                                                                                                                                                                      STRAIN-CV. PIONEER 3184; TISSUE-Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118575 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATHWAY: Sucrose synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9FF17;
15-JUN-2002 (Rel. 41, Created)
                                                                                             01-JUL-1993 (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M97550; AAA33513.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 51.4%;
Best Local Similarity 57.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 419 ARRGVSCHGRYMPR 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ARRGTKCLRREAPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
46 SRDGTRCLREPA 57
                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 1068 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENZYME FUNCTION
                                                                                                                                                                               mays (Maize)
                                                                                                                                                                                                                                  NCBI_TaxID-4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MaizeDB; 25294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALG6_ARATH
ID ALG6_ARATH
                                                                  SPS_MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                          RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                              "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence features of the 1.6 Mb regions covered by twenty physically assigned Pl clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein; Transferase; Glycosyltransferase; Transmembrane;
                                                                          Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiphantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1 - SIMILARITY: BELONGS TO THE ALG6/ALG8 GLUCOSYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                       MEDIJINE-97471969; PubMed-9330910;
Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
Miyajima N., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                              -i- PATHWAY: Glycosylation.
-i- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
         15-JUN-2002 (Rel. 41, Last annotation update)
Probable dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-
glucosyltransferase (EC 2.4.1.-) (Dolichyl-P-Glc:Man9GlcNAc2-PP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79DEC123A6387F26 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 33;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL. POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004856; Alg6_Alg8. Pfam; PF03155; Alg6_Alg8; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB005248; BAB09358.1; -.
EMBL; AX035066; AAK59571.1; -.
                                                dolichyl glucosyltransferase).
AT5G38460 OR MXI10.19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61112 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AY056364; AAL07250.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         reticulum (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                           DNA Res. 4:215-230(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169
204
234
284
380
442
483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Endoplasmic reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256 KCLRRKSP 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 KCLRREAP 13
                                                                                                                                                                   STRAIN-cv. Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            533 AA;
                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214
264
360
422
463
                                                                                                                          NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                      similarity)
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATHWAY: SUCTOSE SYNTHESIS.
SUBUNIT: HOMODIMER OR HOWOTETRAMER (BY SIMILARITY).
PTM: PHOSPHORILATED. HOWEVER, PHOSPHORYLATION IS NOT ESSENTIAL FOR ENZYME FUNCTION (BY SIMILARITY).
SIMILARITY: BELONGS TO THE GLYCOSYLLTRANSFERASE FAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- FUNCTION: INVOLVED IN THE REGULATION OF CARBON PARTITIONING IN THE LEAVES OF PLANTS. MAY REGULATE THE SYNTHESIS OF SUCROSE AND THEREPORE PLAY A MAJON ROLE AS A LIMITING FACTOR IN THE EXPORT OF PHOTOASSIMILATES OUT OF THE LEAF.

-i- CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +
                                                                                                                                                                                                                                  Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Sucrose-phosphate synthase 2 (EC 2.4.1.14) (UDP-glucose-fructose-phosphate glucosyltransferase 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENZIME REGULATION: ACTIVITY REGULATED BY PHOSPHORYLATION AND MODERATED BY CONCENTRATION OF METABOLITES AND LIGHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Characterization of a rice sucrose-phosphate synthase-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB 1; Length 1049;
Pred. No. 65;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             695 698 POLY-GLU.
775 779 POLY-ARG.
1049 Aa; 116455 MW; ED862E2819Aa4B04 CRC64;
                                                                                                                                    15-DEC-1998 (Rel. 37, Last annotation update)
Sucrose-phosphate synthase (EC 2.4.1.14)
(UDP-glucose-fructose-phosphate glucosyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-cv. Indica-IR36; TISSUE-Leaf;
MEDLINE-96235138; PubMed-8666248;
Valdez-Alarcon J.J., Ferrando M., Jimenez-Moraila B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001296; Glycos_transf_1.
Bfam; PF00334; Glycos_transf_1; 1.
Transferase; Glycosyltransferase; Phosphorylation.
DOMAIN 22 29 POLY-GLY.
   PRT; 1049 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1081 AA.
                                                                                                        Last sequence update)
                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U33175; AAC49379.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ARRGIKCLRREAPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 50.0
Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sucrose 6-phosphate.
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   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 170:217-222(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Herrera-Estrella L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-4530;
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004933;
                                                                15-DEC-1998
SPS_ORYSA
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                                DATE THE TARKET TO COLOR COLOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- PATHWAY: Sucrèse synthesis.
-i- SUBUNIT: HOMODIMER OR HOMOTETRAMER (BY SIMILARITY).
-i- PTM: PHOSPHORYLATED. HOMEVER, PHOSPHORYLATION IS NOT ESSENTIAL FOR ENZYME FUNCTION (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
Craterostigma plantagineum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Lamiales incertae sedis; Torenleae;
Craterostigma.
                                                                                                                                                                                                                                                 resurrection plant Craterostigma plantagineum Hochst.";
Plant Physiol. 115:113-121(1997).
-!- FUNCATION: INVOLVED IN THE REGULATION OF CARBON PARTITIONING IN
THE LEAVES OF PLANTS. MAY REGULATE THE SYNTHESIS OF SUCROSE AND
THEREPORE PLAN A MAJON ROLE AS A LIMITING FACTOR IN THE EXPORT OF
PHOTOASSIMILATES OUT OF THE LEAF.
                                                                                                                                                                                       Ingram J., Chandler J.W., Gallagher L., Salamini F., Bartels D.; *Analysis of cDNA clones encoding sucrose-phosphate synthase in relation to sugar interconversions associated with dehydration in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate - UDP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sucrose 6†phosphate.
ENZYME REGULATION: ACTIVITY REGULATED BY PHOSPHORYLATION AND
MODERATED BY CONCENTRATION OF METABOLITES AND LIGHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 1; Length 1081;
Pred. No. 67;
); Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1081 AA; 120933 MW; DD142DC2F1A72900 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001296; Glycos_transf_l.
                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE-97451773; Pubmed-9306694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.0%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Y11795; CAA72491.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                          NCBI_TaxID-4153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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Search completed: July 8, 2003, 16:25:06 Job time: 7.82051 secs

a

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 8, 2003, 16:17:10 ; Search time 30.1538 Seconds (without alignments) 95.665 Million cell updates/sec Run on:

US-09-824-647-7 74 Title: Perfect score: Sequence:

1 ARRGIKCLRREAPR 14

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 seqs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_21:*
:: sp_archea:*
:: sp_bacteria:* Database :

sp_unclassified:*
sp_rvirus:*
sp_bacteriap:* p_invertebrate: sp_vertebrate:* _organelle: rodent: * p mammal:* sp_virus:* sp_fung1:* sp_human:* sp_phage:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

SUMMARIES

			Description	Q9h8s1 homo sapten	Q9d2v3 mus musculu	Q8vjw0 mycobacteri	Q9xgj0 hordeum vul	Q9cyq1 mus musculu	Q922p9 mus musculu	Q9wqq4 rattus norv	043729 homo sapten	Q9d603 mus musculu	Q9sn30 arabidopsis	Q93345 caenorhabdi	Q9zg90 flavobacter	Q9jpd5 rhodocyclus	Q9hna5 halobacteri	Q8qgb6 oncorhynchu	Odvavo homo ganton
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1																			
			a	09н8S1	Q9D2V3	QBVJW0	Q9XGJ0	Q9CYQ1	Q922P9	Q9W0Q4	043729	090603	05NS60	093345	065260	O9JPD5	Q9HNA5	080GB6	048460
			99	4	11	16	10	=	11	11		11			7		11		٧
		Query	Length	413	589	694	78	546	546	130	429	433	1083	327	422	200	831	100	118
	#	Query	Match	91.9	64.9	60.1	58.1	57.4	57.4	55.4	55.4	55.4	55.4	54.1	54.1	54.1	54.1	52.7	52 7
			Score	-89	48	44.5	43	42.5	42.5	41	41	41	41	4	40	40	40	39	5
		Result	No.	-	7	m	4	so	9	7	8	6	10	11	12	13	14	15	9

O31034 mycobacteri O9dcp5 mus musculu O9dxt5 mus musculu O947t9 oryza sativ O8vval burkholderi O8tv46 homo sapien O9ty33 deinococcus O62912 rattus norv P89468 herpes simp O9dyb6 pseudorabie O804056 oryza sativ O9dk03 arelica sp. O91ft0 chilo iride O95014 homo sapien O90703 arabidopsis O49178 oryza sativ O90703 arabidopsis O49178 oryza sativ O90703 arabidopsis O49178 oryza sativ O90704 nanbaena sp O22385 caenorhabdi O8tyt41 anabaena sp O22385 caenorhabdi O8tyt41 anabaena sp O22385 deinococcus O90783 drosophila O905260 mus musculu O90483 drosophila O905483 drosophila	Q9nxx6 homo sapien Q8vds7 mus musculu Q9jlb2 rattus norv
031034 09DCP5 09DCP5 09DCT5 09DCT5 09DCT6 09BVA1 08BVA13 09DYB6 09DYB6 09DYB6 09DYB6 09DYB6 09DYB6 09DYB6 09DYB6 09DYB6 09DYB6 09DYB6 09DYB170 09DY	Q9NXX6 Q8VDS7 Q9JIB2
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190 265 395 395 4452 465 465 300 99 114 114 1134 1157 1157 1157 1157 1157 1157 1157 115	385 400 402
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Arakava T., Shinagawa A., Shibara K., Yoshino M., Itoh M., Ishii Y., Arakava T., Shinagawa A., Shibara K., Yoshino M., Itoh M., Ishii Y., Arakava T., Shara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Redota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomitca M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Ano H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Nyashaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_raxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Adult male kidney CDNA, RIKEN full-length enriched library,
clone:0610012H06, full insert sequence.
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PROSITE; PS00118; PA2_HIS; UNKNOWN_1.
SEQUENCE 589 AA; 63405 MM; IDE8229C413CA292 CRC64;
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Last annotation update)
                                                                       589 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001211; PhospholipaseA2.
Pfam; PF00396; granulin; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-C57BL/63; TISSUE-KIDNEY;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000118; Granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLIZE). 20,
01-MAR-2002 (TrEMBLIZE). 20,
01-JUN-2002 (TrEMBLIZE). 21,
PPE family protein.
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                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                     musculus (Mouse).
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki Y.;
                                                                                                                                 01-JUN-2001
01-JUN-2001
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                                                                    Q9D2V3
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RESULT 2
09D2V3
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ID QB
AC QB
DT QB
DT 011
DE PP
GN MT
GN MT
OC BB
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Omayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Hordeum.
                                                                                                                             Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mueller J., Aeschbacher R.A., Sprenger N., Boller T., Wlemken A., "Carbohydrate-mediated regulation of two key enzymes of fructan synthesis in barley (Hordeum vulgare L.cv. Baraka) leaves."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AJ238715; CAB45560.1;
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                                                                                                                                                                                                                                                                                                                                                                              Length 694;
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Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                    laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AE0070444; AAK46130.1; --
TIGR: MT1857; --
                                                                                                                                                                                                                                                                          INCETTO, ALTONOMICAL PERSONAL DIRENOMICAL PROSITE; PS00449; ATPASE_A; UNKNOWICAL PROSITE; PS00449; ATPASE_A; UNKNOWICAL PS004499 CRC64; CEPURICE 694 AA; 73206 MW; 2FDAD94290A07359 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BC4BF1DB9BE10AD0 CRC64;
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Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                         Score 44.5; DB 16;
Pred. No. 7.7;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CV. BARAKA; TISSUE-PRIMARY LEAF BLADES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                     InterPro; IPR000568; ATPsynt_Asub.
InterPro; IPR000030; Microbac_PPE.
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01-JUN-2001 (TTEMBLEE). 17,
01-JUN-2001 (TTEMBLEE). 17,
01-JUN-2002 (TTEMBLEE). 21,
3930401K13R1k protein.
                                                                                                                                                                                                                                                                                                                                                                              60.18;
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                                                                                                                                                                                                                                                                                                                                                                                                     69.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDC 1551 / OSHKOSH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 RRGTKCL-RREAP 13
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                                                                                                                                                                                                                                                                                                                                                                                                                          9; Conservative
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6
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59715 MW; F5D2090DE1F64723 CRC64;

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546 AA;
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SEQUENCE
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Matches
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Q9WUQ4
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                                                                                                                        SEQUENCE FROM N.A.

C STRING-279BL/63; TISSUB-EMBRYO;

MEDLINE-21085660; PubMed-11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinagawa T., Hara A., Fukunishi Y., Kondo B., Adachi J., Fukuda S.,

A Arakawa T., Hara A., Fukunishi Y., Kondo B., Yamanaka I.,

Salto T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Salto R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsud H.A., Ashburner M., Batalov S., Casavant T.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pescole G., Quackenbush J.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pescole G., Quackenbush J.,

Ruehl P., Satubili F., Suzuki R., Tomita M., Magner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Bolt C., Fletcher C., Fujita M., Garboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Lyons P., Riphyslaw R., Hilly M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Ruzuki H., Toyo-oka K., Wang K. Hasegawa Y., Kawaji H., Kohtsuki S.,

H. Persenter M. Sandoki S., Wangawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
   ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Functional annotation of a full-length mouse cDNA collection. ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC006893; AAH06893.1; --
MGD; MGI:1921272; 3930401K13Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59744 MW; B3AC1562477ABC1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                546 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.4%; Score 42.5; E
52.9%; Pred. No. 14;
tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR0001744; 6PGD.
InterPro; IPR000637; AT_book.
InterPro; IPR000313; PWWP_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001744; 6PGD.
InterPro; IPR000637; AT_hook.
InterPro; IPR000313; PWWP_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF02178; AT_hook; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF02178; AT_hook; 1.
Pfam; PF03446; NAD_binding_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GD; MGI:1921272; 3930401K13R1k.
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152 ADRGSKCLKRAQEQSPR 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AK014456; BAB29363.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ARRGTKCLRR---EAPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00384; AT_hook; 1.
SMART; SM00293; PWWP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIKEN CDNA 3930401K13 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00855; PWWP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          546 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                 NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q922P9
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A10 993289
A20 993289
A33928
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherka; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                     .;
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 DB 11; Length 546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 11; Length 130;
Pred. No. 6.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                     Indels
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Burgess J.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, 297055, CAB09789.1; -.
InterPro; IPR002641; Patatin.
Pfam; PF01734; Patatin; 1.
Pfam; PF01734; Patatin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 130 AA; 14017 MW; A630BA3FCE3A9D9D CRC64;
                                                                                                                                                                                                                                                               UL-NUV-1999 (TrEMBLrel. 12, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) Secretory leukocyte protease inhibitor.
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Last annotation update)
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Score 42.5; Di
Pred. No. 14;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00317; 4_DISULFIDE_CORE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DJ388M5.4 (putative GS2 like protein).
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01-JUN-1998 (TIEMBLEEL: 06, Created)
01-JUN-1998 (TIEMBLEEL: 06, Last seq:
01-JUN-2002 (TIEMBLEEL: 21, Last anno
                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                         InterPro; IPR002221; WAP.
Pfam; PF00005; Wap; 2.
PRINTS; PR00003; 4DISULPHCORE.
Probom; PD001224; WAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.4%;
57.4%;
ilarity 52.9%;
Conservative
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38 ARKPAÇCIKREKP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 55.4
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ARRGTKCLRREAP 13
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                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; WAP;
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                   Local Similarity
hes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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NCBI_TaxID=3702;
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092G90;
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093345;
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093345
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                                  REPRETATION OCC
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                                                                                       ö
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
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     DB 4; Length 429;
21;
                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfan; PPO1734; Patatin; 1.
PROSITE; PS00294; PRENTLATION; UNKNOWN_1.
SEQUENCE 433 AA; 48423 MW; 05366ECC8E129A0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TTEMBLrel. 13, Last sequence update)
01-MAR-2002 (TTEMBLrel. 20, Last annotation update)
Sucrose-phosphate synthase-like protein (EC 2.4.1.14).
F28M11.40 OR AT4G10120.
                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1083 AA.
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2; Mismatches
                                                                                       Mismatches
                               Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-C57BL/6J; TISSUE-HEAD;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:1923022; 4833426H19Rik.
InterPro; IPR002641; Patatin.
InterPro; IPR001230; Prenyl_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 409:685-690(2001).
EMBL; AK014771; BAB29543.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                -JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13,
Query Match
Best Local Similarity 70.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                            5 TKCLRREAPR 14
                                                                                                                                                                 1:111: 111
28 TECLRORAPR 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 TKCLRREAPR 14
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28 TQCLRQRAPR 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                            4833426H19R1k protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4833426H19RIK
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Gaps
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                              SEQUENCE FROM N.A.
Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
Mayer K.F.X., Lemcke K., Schueller C.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 327;
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                                                                                                                                                                                                                                                                                            Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                     EU Arabidopsis sequencing project;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1nvestigating biology.";
Science 282:2012-2018(1998).
EBBE; 280215; CAB02276.1; -.
SEQUENCE 327 AA; 37139 MW; BF592D9F0A2FA022 CRC64;
                      Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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Pred. No. 25;
3; Mismatches
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0; Mismatches
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MEDLINE-99069613; PubMed-9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.5%;
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274 SRRFEMCIRRESP 286
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Best Local Similarity 53.00
The Conservative
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Matches 8; Conservative
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*Dark aerobic growth conditions induce the synthesis of a high midpoint potential cytochrome c8 in the photosynthetic bacterium Rubriviax gelatinosus";
Blochemistry 38:15238-15244(1999).
                                         Menin L., Yoshida M., Jaquinod M., Nagashima K.V., Matsuura K.,
Parot P., Vermeglio A.;
                        MEDLINE-20031519; PubMed-10563807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00493; MCM; 1. Probom; PD001041; MCM; 2. SMART; SM00305; HintC; 1. SMART; SM00306; HintN; 1. SMART; SM00350; MCM; 1.
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338 RRATKVWKREAP 349
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Best Local Similarity 61...
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Les 8; Conservative
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01-MAR-2002
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Matches
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                                                                                                         Bacteria; CFB group; Flavobacteria; Flavobacteriaceae; Flavobacterium.
NCBL_TaxID-81421;
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"Primary structure and transcription of genes encoding B870 and
photosynthetic reaction center apoproteins from Rubrivivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mechanisms and effects (Proceedings of the 11th international con photosynthesis), pp.4:2889-2892, Kluwer Academic Publishers,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Phylogenetic analysis of photosynthetic genes of Rhodocyclus gelatinosus: Possibility of horizontal gene transfer in purple horizontal gene transfer in purple
                                                                                                                                                                                           MEDLINE-99051328; PubMed-9831650;
Leng L., Zhu A., Zhang Z., Hurst R., Goldstein J.;
"Cloning, functional expression and purification of endo-beta-
galactosidase from Flavobacterium keratolyticus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   garashi N., Shimada K., Matsuura K., Nagashima K.V.;
Photosynthetic gene cluster in purple bacterium, Rubrivivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhodocyclus gelatinosus (Rhodopseudomonas gelatinosa).
Bacteria; Proteobacteria; beta subdivision; Comamonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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EMBL, AF0818965, AAD04036.1; -

InterPro; IPR003305; CBM Cenc.

InterPro; IPR000757; Glycc_hydro_16.

Pfam: PF02018; CBM 4-9; 1.

SEQUENCE 422 A3; 45783 WW; E072456A740D14AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 2;
Pred. No. 32;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-IL144;
Nagashima K.V., Shimada K., Matsuura K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 269:2477-2484(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Photosyn. Res. 36:185-191(1993)
                                                                  Endo-beta-galactosidase.
Flavobacterium keratolyticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.1%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Conservative
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Best Local Similarity
Matches 7; Conserv
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Q9JPD5;
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Q9JPD5
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MEDLINE-20504483; PubMed-11016950;
MEDLINE-20504483; PubMed-11016950;
MA W.V., Kennedy S.P.; Wahairas G.G., Berquist B., Pan M.,
My W.V., Kennedy S.P.; Wahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung R.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Ebhardt H., Lowe T.W., Liang P., Riley W., Hood L., DasSarma S.;
"Genome sequence of Halobacterium species NRC-1.";
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
RHSSP; P72065; 1AMZ.
IN FROM T.M., Hedgehog hint.C.
InterPro; IPR003586; Hedgehog hint.N.
RISSP: InterPro; IRR001208; MCM.
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                                                                                                                                                                   DB 2; Length 500;
                                                                                                                                                                                                                                  3; Indels
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SEQUENCE 831 AA; 90593 MW; 84A805B091676970 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Halobacterium sp: (strain NRC-1).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
EMBL: AB014704; BAA94021.1; -
InterPro; IPR003695; Ppx_GppA.
Pfam; PF02541; Ppx-GppA; 1.
SEQUENCE 500 AA; 54839 MW; 4D301D723A243DEA CRC64;
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Last annotation update)
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PROSITE; PS50051; MCM_2; 2.
PROSITE; PS00881; PROTEIN_SPLICING; UNKNOWN_1.
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                                                                                                                                                               Score 4'0; DB 2; Pred. No. 37; 2; Mismatches
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RESULT 15
080GB6

CONCORD CONTREMELLED. 21, Created)

DT 01-UUN-2002 (TrEMBLEL). 21, Last sequence update)

OC Concorphyolism mykiss (Rainbow trout) (Salmo gairdneri).

CC Concorphyolism mykiss (Rainbow trout) (Salmo inder) (Salmoniformes; Salmonidae; Oncorhynchus.

CC Actinopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

CC Actinopterygii; Neopterygii; Teleostei; N., O'Farrell C.;

RN SEQUENCE FROM N.A.

RN SEQUENCE FROM N.A.

RN SEQUENCE FROM N.A.

RN SEQUENCE FROM N.A.

RN SEQUENCE TON ARIBOR SANIBA(67.11; "...

CC SEQUENCE TON ARIBOR SANIBA(67.11; "...

CC SEQUENCE TON AAN B4(67.11; "...

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Search completed: July 8, 2003, 16:28:05 Job time : 33.1538 secs

Gaps

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Length 100;

52.7%; Score 39; DB 13; 63.6%; Pred. No. 13; tive 1; Mismatches 3

Query Match 52.7 Best Local Similarity 63.6 Matches 7; Conservative

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